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# FIGURE 1

GCCACGCGTCCGATGGCGTTCACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCT  
 CACTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGAC  
 TGATTACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTAAGTCCCAGAGTA  
 CCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTGTGTCAGCAGAGTGGCTTACACTGGG  
 TCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAG  
 TGGCCCAGGACTCTATGACCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCA  
 GAAGGAAGGATGGTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGG  
 CATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGT  
 GCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGC  
 CTGTGGAATCTGATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACAT  
 TTTTGCTTGTGGAAAGACTGTTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTAT  
 TACGTATAAATTAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAAGTTGCACTTC  
 TTAAGGAACAGCCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTG  
 GAAGCTTTTGTTTATAGGAACCTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAA  
 TTATAAATTAGCTGTAGATATCAGGTGCTTCTGATGAAGTGAAAATGTATATCTGACTAG  
 TGGGAAACTTCATGGGTTTCCTCATCTGTGTCATGTCGATGATTATATATGGATACATTTAC  
 AAAAATAAAAAGCGGGAATTTCCCTTCGCTTGAATATTATCCCTGTATATTGCATGAAT  
 GAGAGATTTCCCATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTTAAGCATA  
 AGTAAACATGATATAAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAAAGCTATT  
 TTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATGCTTACTG  
 TTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTTCAAACT  
 GAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTTAGTGCAATACAATAAACTCT  
 GAAATTAAGACTC

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# FIGURE 3

GGCTCAGAGGCCCCACTGGACCCTCGGCTCTTCCTTGGACTTCTTGTGTGTTCTGTGAGC  
TTCGCTGGATTACAGGGTCTTGGGCATCAGAGGTGAGAGGGTGGGAAGGTCCGCCGCGATG  
GGGAAGCCCTGGCTGCGTGCGCTACAGCTGCTGCTCCTGCTGGGCGCGTCGTGGGCGCGG  
GCGGGCGCCCCGCGCTGCACCTACACCTTCGTGCTGCCCCCGCAGAAAGTTCACGGGCGCT  
GTGTGCTGGAGCGGCCCCGCATCCACGCGGGCGACGCCCCGAGGCCGCCAACGCCAGCGAG  
CTGGCGGCGCTGCGCATGCGCGTCGGCCGCCACGAGGAGCTGTTACGCGAGCTGCAGAGG  
CTGGCGGCGGCCGACGGCGCCGTGGCCGGCGAGGTGCGCGCGCTGCGCAAGGAGAGCCGC  
GGCCTGAGCGCGCGCCTGGGCCAGTTGCGCGCGCAGCTGCAGCACGAGGCGGGGCCCGGG  
GCGGGCCCCGGGGGCGGATCTGGGGGCGGAGCCTGCCGCGGCGCTGGCGCTGCTCGGGGAG  
CGCGTGCTCAACGCGTCCGCCGAGGCTCAGCGCGCAGCCGCCCGGTTCCACCAGCTGGAC  
GTCAAGTTCGCGAGCTGGCGCAGCTCGTCACCCAGCAGAGCAGTCTCATCGCCCGCCTG  
GAGCGCCTGTGCCCCGGGAGGCGCGGGCGGGCAGCAGCAGGTCCCTGCCGCCACCCCCACTG  
GTGCCTGTGGTTCCGGTCCGTCTTGTGGGTAGCACCAGTGACACCAGTAGGATGCTGGAC  
CCAGCCCCAGAGCCCCAGAGAGACCAGACCCAGAGACAGCAGGAGCCCATGGCTTCTCCC  
ATGCCTGCAGGTACCCCTGCGGTCCCCACCAAGCCTGTGGGCCCGTGGCAGGATTGTGCA  
GAGGCCCGCCAGGCAGGCCATGAACAGAGTGGAGTGTATGAACTGCGAGTGGGCCGTGAC  
GTAGTGTGAGTATGGTGTGAGCAGCAACTGGAGGGTGGAGGCTGGACTGTGATCCAGCGG  
AGGCAAGATGGTTTCAGTCAACTTCTTCACTACCTGGCAGCACTATAAGGCGGGCTTTGGG  
CGGCCAGACGGAGAATACTGGCTGGGCCTTGAACCCGTGTATCAGCTGACCAGCCGTGGG  
GACCATGAGCTGCTGGTTCTCCTGGAGGACTGGGGGGGCGGTGGAGCACCTGCCCACTAT  
GATGGCTTCTCCCTGGAACCCGAGAGCGACCACTACCGCCTGCGGCTTGGCCAGTACCAT  
GGTGATGCTGGAGACTCTCTTTCTGGCACAATGACAAGCCCTTCAGCACCGTGGATAGG  
GACCGAGACTCCTATTCTGGTAACTGTGCCCTGTACCAGCGGGGAGGCTGGTGGTACCAT  
GCCTGTGCCCCACTCCAACCTCAACGGTGTGTGGCACCACGGCGGCCACTACCGAAGCCGC  
TACCAGGATGGTGTCTACTGGGCTGAGTTTCGTGGTGGGGCATATTCTCTCAGGAAGGCC  
GCCATGCTCATTCGGCCCCCTGAAGCTGTGACTCTGTGTTCTCTGTCCCCCTAGGCCCTAG  
AGGACATTGGTCAGCAGGAGCCCAAGTTGTTCTGGCCACACCTTCTTTGTGGCTCAGTGC  
CAATGTGTCCCACAGAACTTCCCACTGTGGATCTGTGACCCTGGGCGCTGAAAATGGGAC  
CCAGGAATCCCCCGTCAATATCTTGGCCTCAGATGGCTCCCCAAGGTCATTCATATCT  
CGGTTTGAGCTCATATCTTATAATAACACAAAGTAGCCAC

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## FIGURE 4

MGKPWLRALQLLLLLLGASWARAGAPRCTYTFVLPPQKFTGAVCWSGPASTRATPEAANAS  
ELAALRMVRVGRHEELLRELQRLAAADGAVAGEVRALRKESRGLSARLGQLRAQLQHEAGP  
GAGPGADLGAEPAAALALLGERVLNASAEQAQRAAARFHQLDVKFRELAQLVTQQSSLIAR  
LERLCPGGAGGQQQVLPPPPLVPVVPVRLVGSTSDTSRMLDPAPEPQRDQQTQRQQEPMAS  
PMPAGHPAVPTKPVGPWQDCAEARQAGHEQSGVYELRVGRHVSVWCEQQLEGGGWTVIQ  
RRQDGSVNFFTTWQHYKAGFGRPDGEYWLGLEPVYQLTSRGDHELLVLLEDWGGRGARAH  
YDGFSLEPESDHYRLRLGQYHGDAGDSLWHNDKPFSTVDRDRDSYSGNCALYQRGGWWY  
HACAHSNLNGVWHHGGHYRSRYQDGVYWAEEFRGGAYSLRKAAMLIRPLKL

**Signal peptide:**

Amino acids 1-20

**N-glycosylation sites:**

Amino acids 58-62;145-149

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 97-101

**Tyrosine kinase phosphorylation site:**

Amino acids 441-448

**N-myristoylation sites:**

Amino acids

16-22;23-29;87-93;108-114;121-127;125-131;129-135;187-193;29

3-299;353-359;378-384;445-451;453-459

**Cell attachment sequence:**

Amino acids 340-343

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 418-431

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED



## FIGURE 6

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ  
QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:  
amino acids 1-16

Casein kinase II phosphorylation site:  
amino acids 22-26, 50-54, 113-117

**N-myristoylation site:**  
amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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## FIGURE 7

CGGACGCGTG GGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAG  
GGGAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCG  
CCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCGCTTCGGCTGAAGCA  
TTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCC  
TTGCACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTT  
TCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAA  
TCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGC  
CAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAA  
ATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCC  
GCACAGAGCTTCATAACCTCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATA  
GTTATATTCCAGTCTAAGCCAGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACA  
AATTTGAGAGAATCATCTCTAAGCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCG  
CACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGCTTTTAAAGATGCCTCTCTCTTAAC  
TCTGGGTGGATTTTAACTACAACCTCTTGTCCTCTCGGTGATGGTATTGCTTTGGATTTGT  
TGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCTGAGAAGCTGAGTATCTAT  
GGTGACTTGAGTTTATGAATGAACAAAAGCTAAACAGATATCCAGCTTCTTCTCTTG  
GTTGTTAGATCTAAAACCTGAAGATCATGAAGAAGCAGGGCCTCTACCTACAAAAGTGAAT  
CTTGCTCATTCTGAAATTTAAGCATTTTTCTTTTAAAGACAAGTGTAATAGACATCTAA  
AATTCCACTCCTCATAGAGCTTTTAAAATGGTTTCATTGGATATAGGCCTTAAGAAATCA  
CTATAAAATGCAATAAAGTTACTCAAATCTGTG

## FIGURE 8

MAAPKGSILWVRTQLGLPPLLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQCLTYPLHT  
YPKEEELYACQRCRLFSICQFVDDGIDLNRTKLECESACTEAYSQSDEQYACHLGCQNQ  
LPFAELRQEQLMSLMPKMHLFPLTLVRSFWSMMDSAQSFITSSWTFYLQADDGKIVIF  
QSKPEIQYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGW  
ILTTTLVLVSMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVR  
SKTEDHEEAGPLPTKVNLAHSEI

**Important features:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site:**

amino acids 90-93

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## FIGURE 9

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTC  
TGTTTTTATTCTCTGTCCTATTTGCCATCTCAGAAGTGCGGAGCAAGGAGTCTGTGAGAC  
TCTGTGGGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAA  
GGCATCTGGAGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAAACTCCTTCCAGCTCC  
CACATAAACGTGAGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCT  
CAGGGGAAGACCGTCTTTGGGGTGGACAGATGCCCACTGAAGAGCTTTGGAAGTCAAAGA  
AGCATTCAGTGATGTCAAGACAAGATTTACAACTTTGTGTTGCACTGATGGCTGTTCCA  
TGACTGATTTGAGTGCTCTTTGCTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTT  
TATCACATGTTTAATTACAGTGTTTTACTGCCTGGTAGAACACTAATATTGTGTTATTAA  
AATGATGGCTTTTGGGTAGGCAAACTTCTTTTCTAAAAGGTATAGCTGAGCGGTGAAA  
CCACAGTGATCTCTATTTTCTCCCTTTGCCAAGGTTAATGAACTGTTCTTTTCAAATTCT  
ACTAATGCTTTGAAATTTCAAATGCTGCGCAAAATTGCAATAAAAATGCTATAAA

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## FIGURE 10

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAE  
TGNSFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSKKHSVMSRQDLQTL  
CCTDGCSMTDLSALC

**Important features:**

**Signal sequence:**

amino acids 1-18

**cAMP- and cGMP-dependent protein kinase phosphorylation  
site:**

amino acids 107-111

**N-myristoylation sites:**

amino acids 3-9,52-58,96-102,125-131

**Insulin family signature:**

amino acids 121-136

**Insulin family proteins:**

amino acids 28-46

# FIGURE 11

CCCACGCGTCCGGACAACTGGAGGTGAAAGGAGCTGGTACTGTCCACTGTGCTGTGCGGT  
GCTGAACCTGAGACGCGAGCGGACCAGTTGCTCCAGCACCTGAAGGCAACGCCCTCTTGC  
ACCCCTCTGTGCCCTGTGGGACCCGCTTCACCAACAGGACCCATATCAACTTGACAAAGGA  
GTGTGGTATCGGACGTGGGAGAGAGTCCCTCTGTTTGCCACCTGGGCGCTCATTGAGGCGT  
GACTTTGGAGATTTCTATAGTTTTAGACCAAACTATTTTTTTTTCCCCAGCTAAGACGAT  
CTTTTGAGAGTTTTTTTTTTTTATTGTGATTTATATTTCCACAGCGTTTAGGAATCTTTCT  
GGGGGACTTTTGTGACTGTTAAATAAGGTGAAAAGCAATAAGGATGTTTAAGTGCTGGT  
CAGTTGTCTTGGTTCTCGGATTCATTTTTCTGGAGTCGGAAGGAAGGCCAACCAAAGAAG  
GAGGATATGGCCTTAAATCCTATCAGCCTCTAATGAGATTGCGACATAAGCAGGAAAAAA  
ATCAAGAAAGTTCAAGAGTCAAAGGATTTATGATTCAGGATGGCCCTTTTGGATCTTGTG  
AAAATAAGTACTGTGGTTTGGGAAGACACTGTGTTACCAGCAGAGAGACAGGGCAAGCAG  
AATGTGCCTGTATGGACCTTTGCAAACGTCACTACAAACCTGTGTGTGGATCTGACGGAG  
AATTCTATGAAAACCACTGTGAAGTGCACAGAGCTGCTTGCCTGAAAAACAAAAGATTA  
CCATTGTTCACAATGAAGACTGCTTCTTTAAAGGAGATAAGTGCAAGACTACTGAATACA  
GCAAGATGAAAAATATGCTATTAGATTTACAAAATCAAAAATATATTATGCAAGAAAATG  
AAAATCCTAATGGCGACGACATATCTCGGAAGAAGCTATTGGTGGATCAAATGTTTAAAT  
ATTTTGATGCAGACAGTAATGGACTTGTAGATATTAATGAACCTAAGTGTGATAAAAC  
AGGAAGAACTTGGCAAGGATCTCTTTGATTGTACTTTGTATGTTCTATTGAAATATGATG  
ATTTTAATGCTGACAAGCACCTGGCTCTTGAAGAATTTTATAGAGCATTCCAAGTGATCC  
AGTTGAGTCTGCCAGAAGATCAGAACTAAGCATCACTGCAGCAACTGTGGGACAAAGTG  
CTGTTCTGAGCTGTGCCATTCAAGGAACCCTGAGACCTCCCATTATCTGGAAAAGGAACA  
ATATTATTCTAAATAATTTAGATTTGGAAGACATCAATGACTTTGGAGATGATGGGTCCT  
TGTATATTACTAAGGTTACCACAACTCACGTTGGCAATTACACCTGCTATGCAGATGGCT  
ATGAACAAGTCTATCAGACTCACATCTTCCAAGTGAATGTTCTCCTCCAGTCATCC

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## FIGURE 12

MFKCWSVVLVLGFIFLESEGRPTKEGGYGLKSYQPLMRLRHKQEKNOESSRVKGFMIQDG  
PFGSCENKYCGLGRHCVTSRETGQAECACMDLCKRHYKPVCGSDGEFYENHCEVHRAACL  
KKQKITIVHNEDCFFKGDCKTTEYSKMKNMLLDLQNQKYIMQENENPNGDDISRKKLLV  
DQMFKYFDADSNGLVDINELTQVIKQEELGKDLFDCTLYVLLKYDDFNADKHLALEEFYR  
AFQVIQLSLPEDQKLSITAATVGQSAVLSCAIQGTLRPPIIWKRNNIILNNDLEDINDF  
GDDGSLYITKVTTTHVGNYTCYADGYEQVYQTHIFQVNVPPVI

**Signal sequence:**

Amino acids 1-20

**N-glycosylation site:**

Amino acids 318-322

**Tyrosine kinase phosphorylation sites:**

Amino acids 21-29;211-220

**N-myristoylation sites:**

Amino acids 63-69;83-89;317-323

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 260-271

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## FIGURE 13

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTC  
TGCCCCCTGGACTCCCGTCTCCTCCTGTCCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCA  
GCAGCTTCCCGCGTCTCCGGCGCAGCTTCTCAGCGGACGACCCTCTCGCTCCGGGGCTGA  
GCCCAGTCCCTGGATGTTGCTGAACTCTCGAGATCATGCGCGGGTTTGGCTGCTGCTTC  
CCCGCCGGGTGCCACTGCCACCGCCCGCCGCTCTGCTGCCGCCGTCCGCGGGATGCTCAG  
TAGCCCGCTGCCCGGCCCCCGCGATCCTGTGTTCTCGGAAGCCGTTTGTGCTGCTGCAGAG  
TTGCACGAACTAGTCAATGGTGCTGTGGGAGTCCCCGCGGCAGTGCAGCAGCTGGACACTT  
TGCGAGGGCTTTTGTGCTGCTGCTGCTGCCCGTCTGCTACTCATCGTAGCCCGCCCCG  
GTGAAGCTCGCTGCTTTCCCTACCTCCTTAAGTGAAGTGCCTAACCGCCACCGGCTGGAAT  
TGCTCTGGTTATGATGACAGAGAAAATGATCTCTCCTCTGTGACACCAACACCTGTAAA  
TTTGATGGGGAATGTTTAAGAATTGGAGACACTGTGACTTGCGTCTGTCAAGTGC  
AACAAATGACTATGTGCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTTAC  
CTGCGACAGGCTGCATGCAAACAGCAGAGTGAGATACTTGTGGTGTCAGAAGGATCATGT  
GCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGCTCTGGAGAACTAGT  
CAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAAGTGTGACGAAGATGCC  
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCCTCTGC  
GCTTCTGATGGGAAATCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAA  
CAGGAGAAAATTGAAGTCATGTCTTTGGGTCGATGTCAAGATAACACAACACTACAACACT  
AAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAATGCTAACAAATTAGAA  
GAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT  
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGCAGGTGTGATGCTGGTTAT  
ACTGGACAACACTGTGAAAAAAGGACTACAGTGTTCTTATACGTTGTTCCCGGTCCTGTA  
CGATTTTCAGTATGTCTTAATCGCAGCTGTGATTGGAACAATTTCAGATTGCTGTCATCTGT  
GTGGTGGTCCTCTGCATCACAAAGGAAATGCCCCAGAAGCAACAGAATTCACAGACAGAAG  
CAAAATACAGGGCACTACAGTTCAGACAATACAACAAGAGCGTCCACGAGGTAAATCTAA  
AGGGAGCATGTTTCACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTA  
TAGACAAAAGAATAAGACAAGAGATCTACACATGTTGCCTTGCATTTGTGGTAATCTACA  
CCAATGAAAACATGTACTACAGCTATATTTGATTATGTATGGATATATTTGAAATAGTAT  
ACATTGTCTTGATGTTTTTTCTGTAATGTAAATAAACTATTTATATCACACAATATAGTT  
TTTTCTTTCCCATGTATTTGTTATATATAATAAATACTCAGTGATGAG



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## FIGURE 14

MVLWESPRQCSSWTLCEGFCWLLLLPVMLLIVARPVKLAAFPTSLSDCQTPTGWNC SGY  
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQ  
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED  
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTT TK  
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY  
TGQHCEKKDYSVLYVVP GPVRFQYVLIAAVIGTIQIAVICVVVLCITRK CPRSNRIHRQ  
KQNTGHYSSDNTTRASTRLI

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## FIGURE 15

GGAGCTCAGCCCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGA  
 ATATGATGTCCTCATAGAAGGTGAACTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTA  
 TGACGCCCAGGCACTCTCAGCCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGAT  
 CGGTGTCCTGGACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACG  
 CGTGGAATAATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCT  
 GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAAATTCTCATTGGACTGTACTT  
 CGTGGGCCTGTACAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGT  
 GTTTTTGCACAAGGGCAACTTTTTCTCAGCCAGGAGGAGGGTGCCCTGTGGCATCATTAC  
 AAGTGTCTTGGCATGGGTAAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAA  
 ACCTCAGATGGAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGC  
 TGATGAGACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTTCGGTTCTTGTCCT  
 CCCCCTATTTATTTTTACATTTCTCTATGTGCAAATGAGAAAAACACTAAGGTTTCAGGGA  
 GCAGAGGTATAGCCTTTTCAAGCTTGTTTTTGCCATAATGGTAGTCTTCCTTCTGATGTG  
 GGCGCCCTACAATATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGA  
 CTGCAAGAGCAGCTACAATCTGGACAAAAGTGTTACATCACTAAACTCATCGCCACCAC  
 CCACTGCTGCATCAACCCTCTCCTGTATGCGTTTTCTTGATGGGACATTTAGCAAATACCT  
 CTGCCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACA  
 AGGCACATCGAGGGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAAT  
 GCAAGAAGAATAAACATGGATTTTTCATCTTTCTGCATTATTTTCATGTAAATTTTCTACAC  
 ATTTGTATACAAAATCGGATACAGGAAGAAAAGGGAGAGGTGAGCTAACATTTGCTAAGC  
 ACTGAATTTGTCTCAGGCACCGTGCAAGGCTCTTTACAAACGTGAGCTCCTTCGCCTCCT  
 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAAACCTAAGGCG  
 CGGAAATTTGTCTAAGATCACATAACTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGT  
 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACCTCCAAACCCTGGGGACAAA  
 CGACATGAAATAAATGTATTTTAAAACATCTAAAA



CGGACGCGTGGGCGGACGCGCTGGGCGGCCACGCGCGCGGGCTGGGGCGGTTCGCTTC  
TTCCTTCTCCGTGGGCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCCG  
AAGGGCCTAGTCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCT  
ATCTGGCTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGT  
CATACCTGCCGGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGAC  
AACTTTGGAGGTGGAACAACCTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGT  
GAGACCCGCCTGGTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCAC  
CGCCTGCTGGAGCTGAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTTCACAAGCAGCAGGAG  
GCCCCGGACCTCTTCCAGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGC  
ACCTTCGGGGCCCTCCTGCCTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTAC  
GGGCAGTGTGAAGGAGAAGGGACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGC  
TACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCC  
AGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAA  
TCAAACCTGTTTGAATGCAAGAAGGGCTGGGCCCTGCATCACCTCAAGTGTGTAGACATT  
GATGAGTGTGGCACAGAGGGAGCCAACTGTGGAGCTGACCAATTCTGCGTGAACACTGAG  
GGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGCATGGGGGCAGGGCCA  
GGTCGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAGTGTCTCGATGTG  
GATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAAACAAGCAGTGTGAAAACACCGAGGGC  
GGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTGAAGGAG  
CAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTGCTG  
CAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC  
TTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTCA  
GAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATAATCGCGGCCACCACCT  
GTAGGACCTCCTCCCACCCACGCTGCCCCACAGAGCTTGGGCTGCCCTCCTGCTGGACACT  
CAGGACAGCTTGGTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCA  
GCCCAGTACCCAGGCTTCCTGGGCGAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTG  
GATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAA  
AGTTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTGGTCCTC  
ACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTG  
TGTTACACCATCCCCACACCCATTGCCACTTATTTATTTCATCTCAGGAAATAAAGAAA  
GGTCTTGGAAGTTAAAAA

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## FIGURE 18

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGL  
ERTIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLELSEELVESWW  
FHKQQEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGS  
CDCQAGYGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGP EESNCLQCKKGWALHH  
LKCVDIDECGTEGANCGADQFCVNT EGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVG  
SKCLDVDECETEVC PGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTE  
DELVV LQQMFFGIIICALATLAAKGD LVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

GCCCGGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTT  
AGCTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCT  
TTACCACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCAT  
GAATCTGGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTT  
TGTTCTTATGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTC  
TTCTCTGTTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGA  
TCTTCTCCTGAAACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAA  
TGAAATTTTTAAGGACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGA  
GTTTATCGATGAGCATGCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTC  
CGACAATCGGATTCAAAGTGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAG  
AATTGCCAACAACCCCTGGCACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGC  
GTCCAATCATGAGACAGCCACAACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGC  
TGGCAGACCATTCTCAATGCTGCCAACGACGCTGACCTTTGTAACCTCCCTAAAAAAAC  
TACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTTCACTATGGTGATCTCATATGT  
GGTATATTATGTGAGGCAAAATCAGGAGGATGCCCGGAGACACCTCGAATACTTGAAATC  
CCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAGCACTGTGGTATAGTG  
TCCAAACTGACTGTCAATTGAGAAAAGAAAGAAAGTAGTTTGCGATTGCAGTAGAAATAAGT  
GGTTTACTTCTCCCATCCATTGTAAACATTTGAAACTTTGTATTTTCAAGTTTTTTTTTGAAT  
TATGCCACTGCTGAACTTTTAACAAACACTACAACATAAATAATTTGAGTTTAGGTGATC  
CACCCCTTAATTGTACCCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATTAGT  
TAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTTAATTTAAAAGCAAATAAAAG  
CTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAACA



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## FIGURE 21

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTTCCACTT  
 TGTTGAATTGTTCTTATACTCAAAATTGCACCAAGACACCTTGTCTCCCAAATGCAAAAT  
 GTGAAATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTG  
 TCACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAATG  
 CTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCA  
 GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATG  
 CAAACTGCCATTTAGATAATGTCTGTATAGCTGCAAAATATTAATAAACTTTAACAACAAA  
 TCAGATCCATAAAAGAACCTGTGGCTTTGCTACAAGAGTCTATAGAAATTTCTGTGACAG  
 ATCTTTCACCAACAGATATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTAC  
 TAGGTTACAAGAACAACACTATCTCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTG  
 AATTTGTAAAAACCGTGAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGT  
 TATCTGTGAATCATAGGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTA  
 CTTTAAGGATATCCCAGAGCTTCCAAAAGACCACAGAGTTTGATACAAATTCACCGGATA  
 TAGCTCTCAAAGTTTTCTTTTTTGATTATATAACATGAAACATATTCATCCTCATATGA  
 ATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG  
 GCAATGTTGCAGTTGCATTTTTTATATTATAAGAGTATTGGTCCTTTGCTTTCATCATCTG  
 ACAACTTCTTATTGAAACCTCAAATTTATGATAATTCTGAAGAGGAGGAAAGAGTCATAT  
 CTTCAGTAATTTTCACTCAATGAGCTCAAACCCACCCACATTATATGAACTTGAAAAAA  
 TAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGAGTCTATGTGCATTTT  
 GGAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT  
 ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCAATTTTGA  
 TGTCCTCTGGTCCTTCCATTGGTATTAAGATTATAATATTCTTACAAGGATCACTCAAC  
 TAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTTACCTTCTGGTTCTTCA  
 GTGAAATTCAAAGCACCAGGACAACAATTCACAAAATCTTTGCTGTAGCCTATTTCTTG  
 CTGAACTTGTTTTTCTTGTGTTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA  
 TTGCCGGAAGTGTACACTACTTCTTTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGCA  
 TACATCTCTATCTCATTTGTTGTGGGTGTCTCTACAACAAGGGATTTTGCACAAGAATT  
 TTTATATCTTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTTCGGCAGCACTAGGAT  
 ACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAACAACCTTTATTTGGA  
 GTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCATCA  
 TATACAAAGTTTTTTCGTCACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA  
 TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCCTTCTCGGCACCACCTGGATCT  
 TTGGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCA  
 ATGCTTTCCAGGGGATGTTCAATTTTTTTTATTCTGTGTGTTTTATCTAGAAAGATTCAAG  
 AAGAATATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAGGTAAACAT  
 AGAGAATGGTGGATAATTACAACCTGCACAAAAATAAAAAATTCCAAGCTGTGGATGACCAA  
 TGTATAAAAAATGACTCATCAAATTATCCAATTATTAATACTAGACAAAAAGTATTTTAA  
 ATCAGTTTTTCTGTTTATGCTATAGGAACTGTAGATAATAAGGTAAAATTATGTATCATA  
 TAGATATACTATGTTTTTCTATGTGAAATAGTTCTGTCAAAAAATAGTATTGCAGATATTT  
 GGAAAGTAATTGGTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTA  
 ACACGAGAAGTATATGAATGTCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGT  
 GTTGCCCTTTGAAACTAGTCCCCCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAA  
 CATAAGAGAATGAAGGGGCAGAAATATCAAACAGTGAAAAGGGAATGATAAGATGTATTTT  
 GAATGAACTGTTTTTTCTGTAGACTAGCTGAGAAATTGTTGACATAAAATAAAGAATTGA  
 AGAAACACATTTTACCATTTTGTGAATTGTTCTGAACTTAAATGTCCACTAAAACAACCTT  
 AGACTTCTGTTTGCTAAATCTGTTTCTTTTTCTAATATTCTAAAAAAGGTTT  
 ACCTCCACAAATTGAAA



## FIGURE 22

MKRLPLLVVVFSTLLNCSYTNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDN  
 ECGNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNV  
 CIAANINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSSLGYKNNTI  
 SAKDTLSNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSF  
 QKTTEFDTNSTDIALKVFFFDSDYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAF  
 YYKSIGPLLSSSDNFLKPKQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHR  
 KVTDRYRSLCAFWNYSPDTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIG  
 IKDYNILTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVG  
 INTNTNKLFCSIIAGLLHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLS  
 PAVVVGFSAAALGYRYYGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHT  
 AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFI  
 FLFLCVLSRKIQEEYYRLFKNVPCCFGCLR

CTCTCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGC  
CTTAAATTTTCAGCTCATCACCTTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGAT  
CCTTGCCATTTGCACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGG  
GGGCCTCCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGT  
GTGTGATGACGGCTGGGACATTAAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGG  
AGCTGCCAGCGGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAA  
GGTCCTCATCCAATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCA  
AGAAGAAGTTTATGATTGTTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGA  
GAGCTCTTTCTCCCCAGTCCCAGAGGGGTGTCAAGCTGGCTGACGGCCCTGGGCATTGCAA  
GGGACGCGTGGAAGTGAAGCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAG  
CCTCCGGGGCCGCAAAGGTGGTGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCA  
AAAACGCTGCAACAAGCATGCCTATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATG  
CTCAGGACGAGAAGCAACCCTTCAGGATTGCCCTTCTGGGCCCTTGGGGGAAGAACACCTG  
CAACCATGATGAAGACACGTGGGTGCAATGTGAAGATCCCTTTGACTTGAGACTAGTAGG  
AGGAGACAACCTCTGCTCTGGGCGACTGGAGGTGCTGCACAAGGGCGTATGGGGCTCTGT  
CTGTGATGACAACTGGGGAGAAAAGGAGGACCAGGTGGTATGCAAGCAACTGGGCTGTGG  
GAAGTCCCTCTCTCCCTCCTTCAGAGACCGGAAATGCTATGGCCCTGGGGTTGGCCGCAT  
CTGGCTGGATAATGTTCTGTTGCTCAGGGGAGGAGCAGTCCCTGGAGCAGTGCCAGCAG  
ATTTTGGGGGTTTTCAGACTGCACCCACCAGGAAGATGTGGCTGTCTATCTGCTCAGTGTA  
GGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAAGAAAAACACAGAGAAGGGAGC  
ATTTACTGTCTACATGACTGCATGGGATGAACACTGATCTTCTTCTGCCCTTGGACTGGG  
ACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGGATCAGAACTTACAACATC  
AGGTCTAGTTCTCAGGCCATCAGACATAGTTTCCAGCCTCCATAATTGTGTGTATCAACTACTTAAATA  
TCCACATTGCACACAGCAGATTTCCAGCCTCCATAATTGTGTGTATCAACTACTTAAATA  
CATTTCTCACACACACACACACACACACACACACACACACATACACCATTTGTCC  
TGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGATTCTAGAGGA  
ACGGAATTTTAAAGGATAAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTGGCTCTATA  
ATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAGATAGCACTATGTG  
TTCAAA

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## FIGURE 24

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAV  
LCRELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDA  
GASCENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLG  
CGRAVLTQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECED  
PFDLRLVGGDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKC  
YGPVGRIWLDNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site:**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site:**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site:**

amino acids 196-200

**Speract receptor repeated domain signature:**

amino acids 29-67, 249-287

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## FIGURE 25

CGGACGCGTGGGCGTCCGGCGGTGCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTG  
GGCCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGCGCATGTCCACTGGGG  
CTACTGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGTGGG  
CGCCGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTAC  
TGCCAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG  
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGAC  
TTCTGGGACTTCTGCCTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCAT  
GGAGGTCTGATCTATCCAGTCTTGGGAACGTACTGGGACAACGTAAACCGTTGCACCTGC  
CAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAA  
CTATGGCTGGCAGGCTGGGAACACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCAT  
TCGCTACCGCCTGGGCACCATCCGCCCCTTCTCGGTCATGAACATGCATGAAATTTA  
TACAGTGCTGAACCCAGGGGAGGTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCC  
CAACCTGATTCATGAGCCTCTTGACCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCAC  
AGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACACATGACGCCTGTCTT  
GTCGCCCCAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG  
TCTCGATGGTGCTGGTGGTTCTTGCCTCGCCGAGGGGTGGTGTCTGACCACTGCTACCC  
CTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCG  
AGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGCCCAACAGCTATGTTAATAA  
CAATGACATCTACCAGGTCACCTCTGTCTACCGCCTCGGCTCCAACGACAAGGAGACTTCTT  
GAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGATGAGGACTTCTT  
CCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATA  
CCGCCGGCATGGGACCCACTCAGTCAAGATCAAGGATGGGGAGAGAGACGCTGCCAGA  
TGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCCAGCCTGGGGCGAGAG  
GGGCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAGAGCTTCGTGCTGGG  
CGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTGCGGGCACACGC  
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATGGGGCGGTGAC  
CCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGGCGC  
GGGTTCCGCTGACGCAGCGCCCCGCCTGGGAGCCGCGGGCAGGCGAGACTGGCGGAGCCC  
CCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAGATCC  
CAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC  
CAATACCCCAACCAATCCCGTATTCTTTTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTT  
CAAGTGACCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACC  
TGGCTAATTTTTGTATTTTTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTT  
CGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGG  
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCAC  
TGTTTTAAATAAAACCAAAGTATTGATAAAAAAAA

## FIGURE 26

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRAD  
DCALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWD  
NCNRCTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**N-glycosylation site:**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site:**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site:**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site:**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site:**

amino acids 398-409

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## FIGURE 27

CCCACGCGTCCGGCAGGTTTTTCTTCAAGCCAAGAAGGACACGGATTGGCTGAAGGAGAA  
 AGTGCAGAGCTTGCAGACACTGGCTGCCAACAACCTCTGCGTTGGCCAAAGCCAACAACGA  
 CACCCTGGAGGATATGAACAGCCAGCTCAACTCATTACAGGTCAGATGGAGAACATCAC  
 CACTATCTCTCAAGCCAACGAGCAGAACCCTGAAAGACCTGCAGGACTTACACAAAGATGC  
 AGAGAATAGAACAGCCATCAAGTTCAACCAACTGGAGGAACGCTTCCAGCTCTTTGAGAC  
 GGATATTGTGAACATCATTAGCAATATCAGTTACACAGCCCACCACCTGCGGACGCTGAC  
 CAGCAATCTAAATGAAGTCAGGACCCTTGCACAGATACCTTACCAAACACACAGATGAT  
 CTGACCTCCTTGAATAATACCCTGGCCAACATCCGTTTGGATTCTGTTTCTCTCAGGATG  
 CAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATTATG  
 GAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATACTA  
 CAAGGTCCACCGGGCCCCAGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGC  
 CCAACTGGCAACAAGGGACAGAAAGGAGAGAAGGGGGAGCCTGGACCACCTGGCCCTGCG  
 GGTGAGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCT  
 AAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGC  
 CCCAGTGGGGACCCAGGCCCCCCGGGCCACCAGGCAAAGAGGGACTCCCCGGCCCTCAG  
 GGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCCTGGACCT  
 CGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCAAGGGCCCCCGGGC  
 CCTCCTGGCCCATCAGGAGCGGTGGTGCCCTGGCCCTGCAGAATGAGCCAACCCCGGCA  
 CCGGAGGACAATAGCTGCCCGCCTCACTGGAAGAAGCTTTCTGTGAAGACAAGTCTTCACAT  
 TCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACAT  
 CTTGTTTTTCATAAACACTAGAGAGGAACAGCAATGGATAAAAAAACAGATGGTAGGGAGA  
 GAGAGCCACTGGATCGGCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGAT  
 GGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGC  
 CATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAAACGATTTCCAA  
 TGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCTGCA  
 TTATAACGGACTGTGATGGGATCACATGAGCAAATTTTCAGCTCTCAAAGGCAAAGGACA  
 CTCCTTTTCTAATTGCATCACCTTCTCATCAGATTGAAAAAAAAAAGCACTGAAAACCAA  
 TTAAGTAAAAAATTTGACAGCTAGTGTTTTTTTACCATCCGTCATTACCCAAAGACTTGG  
 GAACTAAATGTTCCCCAGGGTGATATGCTGATTTTCATTGTGCACATGGACTGAATCAC  
 ATAGATTCTCCTCCGTGAGTAACCGTGCGATTATACAAATTATGTCTTCCAAAGTATGGA  
 AACTCCAATCAGAAAAAGGTTATCATTTGGTCGTTGAGTTATGGGAAGAACTTAAGCATA  
 TACTGTGTAAACAGTGCCATACATTTCTAAAATCCCAAGTGTAGGAAAAATATGCAGACA  
 TACAGATATATAGGCCAACTATTAGTAATAATATGAAATATACTTAAAGAGCTTTTAAAA  
 CTTTGTATTTTTGTACAAAAAAA

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## FIGURE 28

MQQDLMRSRLDTEVANLSVIMEEMKLVD SKHGQLIKNFTILQGPPGPRGPRGDRGSQGPP  
GPTGNKGQKGEKGEPPGPPGAGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQ  
GPSGDPGPPGPPGKEGLPGPQGPFGQLQGT VGEPPGPRGLPGLPGVPGMPGPKGPP  
GPPGPPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSS  
HLVFINTREEQQWIKKQMVGRESHWIGLTD SERENEWKWLDGTSPDYKNWKAGQPDNWDGH  
GHGPGEDCAGLIYAGQWDFQCEDVNNFICEKDRET VLSAL

**Signal sequence:**

None

**Transmembrane domain:**

None

**N-glycosylation site:**

16-19, 37-40, 213-216

**Tyrosine kinase phosphorylation site:**

212-220

**N-myristoylation site:**

97-102, 100-105, 148-153, 267-272, 293-298, 310-315

**Cell attachment sequence:**

51-53

**C-type lectin domain signature:**

308-330

**Lectin C-type domain:**

233-330

**Collagen triple helix repeat:**

43-102, 127-186

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## FIGURE 29

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACT  
GTGTTGAAGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACAC  
AGTGTCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTA  
GGAGGACTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCCATGAAGG  
AGTATGTGCTCCTATTATTCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCAC  
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATG  
ATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCAACAAGAGAGCCAAGAA  
GCCATTTTTTTCCATTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGTCTATTTCAC  
GAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATA  
CTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG  
GACTCACTTCACTTTATGGTCTGATCCTGAACAACAACAAGCTAACGAAGATTCACCCAA  
AAGCCTTTCTAACCAACAAGAAGTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTG  
AAATACCACTTAATCTTCCCAAATCATTAGCAGAATCAGAATTCATGAAAATAAAGTTA  
AGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTTGGAATAGATG  
CAAACCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTTC  
ATATCAGAATTGCAGAAGCAAAACTGACCTCAGTTCCTAAAGGCTTACCACCAACTTTAT  
TGGAGCTTCACTTAGATTATAATAAAATTTCAACAGTGGAAGTTGAGGATTTTAAACGAT  
ACAAAGAACTACAAAGGCTGGGCCTAGGAAACAACAATAACAGATATCGAAAATGGGA  
GTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACAATAAACTAAAAAAA  
TCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCCTTCATTCTAATTCAA  
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTAT  
ACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACAT  
TTCGTTGTGTTTTGAGCAGAATGAGTGTTTCAGCTTGGGAACTTTGGAATGTAATAATTAG  
TAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATTTGGAATACTTGAAC  
TCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGTAAGTCC  
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATTGATACATAAG  
GGGTTGAGAGAAACAAGCATCTATTGCAGTTTCTTTTTTGCGTACAAATGATCTTACATA  
AATCTCATGCTTGACCATTCTTTCTTCATAACAAAAAAGTAAGATATTCGGTATTTAAC  
ACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACTTAGC  
AAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA  
AGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT  
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCC  
GTCTTTATGTTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTCAATTACCAAC  
TTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTA  
ATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAAC  
CGCATTTTAATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATTGTTAGGCATATA  
ACATTGCCACTTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTG  
GAAGAGCCTGGACACTAACAATTCTACACCAAATTGTCTCTTCAAATACGTATGGACTGG  
ATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACA  
GAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAA  
CATATGTAAATCAGAAAACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT





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## FIGURE 31

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA  
 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC  
 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG  
 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA  
 GAAGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGGGATCACCTTTGTGAGCAAAAAG  
 GCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT  
 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT  
 GGCTGGGTTGGAGATGGATTCTGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG  
 AAAATGGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT  
 TGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAA  
 GATCCCATATTCAACACTCAAACCTGCAACACAAACAAGAGATTTATTGTTCAGTGACAGT  
 ACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT  
 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG  
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAG  
 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCCTCTTC  
 TTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT  
 TTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAG  
 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAGAGTCC  
 AAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA  
 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA  
 ATCAAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTTGTTTCTTAATGGAATCAGC  
 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAATGCCCTTCTCCTTATTGTAAC  
 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTCTCTAGCCTGGCTAT  
 GTCCTAATAATATCCCCTGAGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTAAAACATC  
 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC  
 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCCTTCTTCA  
 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA  
 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA  
 TCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCA  
 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT  
 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT  
 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCT  
 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA  
 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC  
 TGTAATTGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT  
 TTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTATTATTTTGCTGA  
 GACTAATCTTATTCATTTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAAC  
 ATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAA  
 CAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATT  
 TGTGACAAAAAATTAAAGCATTTAGAAAACCT

## FIGURE 32

MARCFSLVLLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA  
CRLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPV  
SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA  
PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTAL  
LVLALLFFGAAAGLGFCYVKRYVKAFPFNTNKNQQKEMIETKVVKEEKANDSNPNEESKKT  
DKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site:**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site:**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site:**

amino acids 79-88

**N-myristoylation site:**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259



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TCTACTTATGTTGGACACTTGGCAGAAGGACCGTGCCCGGCGGCCTCATTTTGACCAGCT  
GGTGGCTGCATTTGACAAGATGATCCGCAAGCCAGATACCCTGCAGGCTGGCGGGGACCC  
AGGGGAAAGGCCTTCCCAGGCCCTTCTGACCCCTGTGGCCCTGGACTTTCCTTGCTGGA  
CTCACCCCAGGCCTGGCTTTCAGCCATTGGACTGGAGTGCTACCAGGACAACTTCTCCAA  
GTTTGGCCTCTGTACCTTCAGTGATGTGGCTCAGCTCAGCCTAGAAGACCTGCCTGCCCT  
GGGCATCACCTGGCTGGCCACCAGAAGAAGCTGCTGCACCACATCCAGCTCCTTCAGCA  
ACACCTGAGGCAGCAGGGCTCAGTGGAGGTCTGAGAATGACGATACCCGTGACTCAGCCC  
TGGACACTGGTCCGAGAAGGGACATGTGGGACGTGAGCCGGGCTCCAACAGCCTCTGTGA  
GAGATGCCCCACACCAAACCCAACCCTCCGATGGCTGCATTCCCTGGTCCTCCGCTTTTC  
CACCAGCCCCCTCCTCATTAAGGGAAAGAAGGGAATTTGCAAAAAAAAAAAAAAAAAAAAA  
AAAAAAA

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## FIGURE 34

MATEGAAQLGNRVAGMVCSLWVLLLVS SVLALEEVLLDTTGETSEIGWLTYPPGGWDEVS  
VLDDQRRLLTRTFEACHVAGAPPGTGQDNWLQTHFVERRGAQRAHIRLHFSVRACSSLGVS  
GGTCRETFTLYYRQAEEDSPDSVSSWHLKRWTKVDTIAADESFPSSSSSSSSSSSSSSAAW  
AVGPHGAGQQRAGLQLNVKERSFGPLTQRGFYVAFQDTGACLALVAVRLFSYTCPAVLRSF  
ASFPETQASGAGGASLVAAVGTCVAHAPEEDGVGGQAGGSPPRLLHCNGEGKWMVAVGGC  
RCQPGYQPARGDKACQACPRGLYKASAGNAPCSPCPARSHAPNPAAPVPCPCLEGFYRASS  
DPPEAPCTGPPSAPQELWFEVQGSALMLHWRLPRELGGRGDLLFNVVCKECEGRQEPASG  
GGGTCHRCRDEVHFDPRQRGLTESRVLVGGRLAHVPYILEVQAVNGVSELSPDPPQAAAI  
NVSTSHEVPSAVPVVHQVSRASNSITVSWPQPDQTNGNILDYQLRYYDQAEDESHSFTLT  
SETNTATVTQLSPGHIYGFQVRARTAAGHGPYGGKVYFQTL PQGELSSQLPERLSLVIGS  
TLGALAFLLLAITVLAVVFQRKRRTGYTEQLQQYSSPGLGVKYYIDPSTYEDPCQAIR  
ELAREVDPAYIKIEEVIGTGSFGEVRQGRQLQPRGRREQTVAIQALWAGGAESLQMTFLGR  
AAVLGQFQHPNILRLEGVVTKSRLPLMLVTEFMELGPLDSFLRQREGQFSSLQLVAMQRGV  
AAAMQYLSSFAFVHRSLSAHSVLVNSHLVCKVARLGHSPQGPSCLLRWAAPEVIAHGKHT  
HVGSDDELWRTALLGHE

### signal sequence:

Amino acids 1-31

### Transmembrane domains:

Amino acids 217-234;598-618

### N-glycosylation site:

Amino acids 481-485

### Glycosaminoglycan attachment sites:

Amino acids 249-253;419-423

### cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 66-70;150-154;624-628

### Tyrosine kinase phosphorylation sites:

Amino acids 644-673;664-671

### N-myristoylation sites:

Amino acids 10-16;15-21;79-85;99-105;118-124;188-194;  
192-198;218-224;250-256;261-267;275-281;276-282;298-304;321-  
327;328-334;420-426;421-427;440-446;449-455;599-605;626-632;  
708-714;766-772;779-785

### Amidation site:

Amino acids 693-697

### Cell attachment sequences:

Amino acids 310-313;399-402

# FIGURE 35

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTAC  
GCATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGAC  
TTGTGTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCAC  
TGGTGTGTTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTG  
CCTGCACCAGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGT  
CGACCGCAGCCTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTTCGACACGGGGCTCGGAG  
TCCTCTCAAGCCGCTCCCGCTGGAGGAGCAGGTAAGTGGAAACCCCGAGCTATTAGAGGT  
CCCACCCCAAACCTCAGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATA  
TTCTCCTTACGACTCTCAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCA  
GCTGACCAAGGTGGGCATGCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTA  
TGTGGAAGACATTCCCTTTCTTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTT  
CACTAACATTTTTTCGGAATCTGGAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTG  
TCAGAAAGAAGGACCCATCATCATCCACACTGATGAAGCAGATTGAGAAGTCTTGTATCC  
CAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTC  
TTTACAGCCAGGAATCTCAGAGGATTTGAAAAAGGTGAAGGACAGGATGGGCATTGACAG  
TAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGCCGAGCAGGCACACAA  
CCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACAGAGAGCTGTGGA  
CACATCCTTGTAATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGCAGTAGGCC  
ATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGCCCCGA  
CAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTTAAT  
GACCCTGGGGATTTTTTGACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAC  
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCA  
GGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATGTC  
AGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGA  
AGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAATAAAGT  
GCCTTTATACAATG

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## FIGURE 36

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMOVVFRHG  
ARSPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMF  
AGQLTKVGMQOMFALGERLRKKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGL  
FQCQKEGP IIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISED LKKVKDRMG  
IDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA  
VGPFLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLT  
MELYQHLESKEWFVQLYHKGQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQ  
VMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 218-222

**Casein kinase II phosphorylation site:**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site:**

amino acids 280-288

**N-myristoylation site:**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site:**

amino acids 216-220

**Leucine zipper pattern:**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature:**

amino acids 50-65



## FIGURE 37

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCG  
 ACCCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCC  
 GAAGGTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCCTGCTGTTCCGGCTG  
 CCTGGGCGTCTTCGGCCTCTTCGGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCG  
 GAATGCTGTGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGT  
 CTTCTATGCTGCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGA  
 GCTCATCAGAGAACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTT  
 GGTGACCTTCGACCTCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCA  
 GTGCTTTGGCTATGTGACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCAT  
 CATGGACACCACAGTGGATGTGGACAAGAGGGTTCATGGAGACAACTACTTTGGCCCAGT  
 TGCTCTAACGAAAGCACTCCTGCCCCCCTCATGATCAAGAGGAGGCAAGGCCACATTGTGCG  
 CATCAGCAGCATCCAGGGCAAGATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAA  
 GCACGCAACCCAGGCTTTCTTTGACTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGA  
 GGTGACCGTCATCAGCCCCGGCTACATCCACACCAACCTCTCTGTAAATGCCATCACCGC  
 GGATGGATCTAGGTATGGAGTTATGGACACCACCACAGCCCAGGGCCGAAGCCCTGTGGA  
 GGTGGCCCAGGATGTTCTTGCTGCTGTGGGGAAGAAGAAGAAAGATGTGATCCTGGCTGA  
 CTTACTGCCTTCCTTGGCTGTTTATCTTCGAACTCTGGCTCCTGGGCTCTTCTTCAGCCT  
 CATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCCAAGAACTCCTTAGTACTCTGACCAGCC  
 AGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGCTTACTCTACAAGGGACAGTTGCAT  
 TTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGGAAAGACTGAAGAAACACATCTC  
 GTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACAAGCTTCTTCCCAGGGTGAGG  
 GGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACTAAAACTAGAAATAAACA  
 TCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAG  
 CTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

## FIGURE 38

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAA  
GAKLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAIVAAAAEILQCFGY  
VDILVNNAGISYRGTIMDITVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIS  
QGKMSIPFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSR  
YGVMDTTTAQGRSPVEVAQDVLAAGVKKKKDVLADLLPSLAVYLRRLAPGLFFSLMASR  
ARKERKSKNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site:**

amino acids 228-232

**Glycosaminoglycan attachment site:**

amino acids 47-51

**Casein kinase II phosphorylation site:**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site:**

amino acids 145-153, 146-153

**N-myristoylation site:**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site:**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 6-17

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## FIGURE 39

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGT  
GTACCGCCTCTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACAC  
CGTCTACTACGTGCACAACATCAAGTTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGG  
CTACCGCACCTACCGCTGTGCCCCACCCCTGGCCACACTCTTCAAGATCCTGGCGTCCCTTACAT  
CAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTGGTGGATGCTACGGCGCTCCCT  
CAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAGCGACATCCCCGACGTCAAGAA  
CGACTTCGCCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAAGCGCTTCGCCGT  
CTTCTGTGCGGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCTGGA  
CAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAG  
TGGCATCCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGA  
CGTGACCATCCCGCCAGCATTTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTCTACCACACAGC  
GGCCAAGATTGAAGCGCCTGCGCTGGCCTTCTGCGCGAGAACCCTGCGGGCGCTGCACATCAAGTT  
CACCGACATCAAGGAGATCCCGCTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGAC  
GGGCAACCTGAGCGCGGAGAACAAACCGCTACATCGTCATCGACGGGCTGCGGGAGCTCAAACGCCT  
CAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCACAGATGTGGCGTGCA  
CCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAAGAAGAT  
GGCGAACCTGAGCTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAG  
CCTCCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAG  
CTTCCAGCACCTGCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCAT  
CCAGATCGGCAACCTCACCAACCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCC  
CACCCAGCTCTTCTACTGCCGAAGCTGCGCTACCTGGACCTCAGCCACAACAACCTGACCTTCTT  
CCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCTAGCCATCACGGCCAACCGGATCGAGAC  
GCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCTGGGCAACAACGTGCTGCA  
GTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGCAACCGGCT  
GGAGTGCTGCTGTGGAGCTGGGCGAGTGGCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGC  
CTGAGCGAGGCGCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGC  
AGGCCTAGCTTCTCCAGAACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCAGGAGCCTGGGG  
CCGCTTGTGAGTCAGGCCAGAGCGAGAGGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCCTCTGA  
GACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATA  
ATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCTTGGGA  
CCCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCCAGATAACTTATA  
CATTTCCCAAGAAAGTTTCAGCCCAGATGGAAGGTGTTTCAGGGAAAGGTGGGCTGCCTTTTCCCTTG  
TCCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCG  
AACCAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGC  
AGGCCTCCAGCTGGAAAGGCCAGGCCTGGAGCTTGCCCTCTCAGTTTGTGGCAGTTTTAGTTTTT  
TTGTTTTTTTTTTTTTTAATCAAAAAACAATTTTTTTTAAAAAAAAGCTTTGAAAATGGATGGTTT  
GGGTATTA AAAAGAAAAAAACTTAAAAAAAAGACACTAACGGCCAGTGAGTTGGAGTCTC  
AGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGTTGAACTGTGTTTCTTTCCCTGGG  
CGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTGGTCCAGGAGTTCTATTTGTTTCTGGG  
GAGGGAGGTTTTTTTTGTTTTGTTTTTGGGTTTTTTTTGGTGTCTTGTTTTCTTCTCCTCCATGTGT  
CTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAG  
GAGACTCGGGTTGGCTAATCCCCGATGAACGGTGCTCCATTCGCACCTCCCCTCCTCGTGCTGC  
CCTGCCTCTCCACGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCA  
CCTCCTGCGGCATGGGTGTGTCCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGC  
ACCTGGTCCTTCATGAAGAGCAGACACTAGAGGTGGTGGGAGGTGCGGAGGTGCGCCCTGGGAG  
GGCAGGCGTTGAGTTCCAAGCCGTTCCCGTCCCTGGCGCTGGAGTGACACAGCCAGTCGGCAC  
CTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTTAGAAGGGTCCCCGCCTTA  
GATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGTCCATCCGTC  
TGTCCGTCCATTTGTGTTTTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTA  
TCAAATAAAATCTATAACAGAAAAA

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## FIGURE 40

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASF  
YISLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDP  
LYSKRFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSIGIPDTVFD  
LVELEVLKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTD  
IKEIPLWIYSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTD  
VGVHLQKLSINNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDN  
NLKTIEEIIISFQHLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYC  
RKLRYLDSLHNNLTFLPADIGLLQNLQNLAITANRIETLPPELFFQCRKLRLHLGNNVLQ  
SLPSRVGELTNLTQIELRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWR  
ADKEQA

**Transmembrane domain:**  
amino acids 51-75 (type II)

**N-glycosylation site:**  
amino acids 262-266, 290-294, 328-332, 396-400, 432-436,  
491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**  
amino acids 85-89

**Casein kinase II phosphorylation site:**  
amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site:**  
amino acids 173-179, 261-267, 395-401, 441-447

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## FIGURE 41

GGGGGAGAAGGCGGCCGAGCCCCAGCTCTCCGAGCACCGGGTCGGAAGCCGCGACCCGAG  
CCGCGCAGGAAGCTGGGACCGGAACCTCGGCGGACCCGGCCCCACCCAACCTCACCTGCGC  
AGGTCACCAGCACCCCTCGGAACCCAGAGGCCCGCGCTCTGAAGGTGACCCCCCTGGGGAG  
GAAGGCGATGGCCCCCTGCGAGGACGATGGCCCCGCGCCCGCTCGCCCCGGCCGGCATCCC  
TGCCGTTCGCCTTGTGGCTTCTGTGTCACGCTCGGCCTCCAGGGCACCCAGGCCGGGCCACC  
GCCCCGCGCCCCCTGGGCTGCCCCGCGGGAGCCGACTGCCTGAACAGCTTTACCGCCGGGGT  
GCCTGGCTTCGTGCTGGACACCAACGCCTCGGTGAGCAACGGAGCTACCTTCCTGGAGTC  
CCCCACCGTGCGCCGGGGCTGGGACTGCGTGCGCGCCTGCTGCACCACCCAGAACTGCAA  
CTTGGCGCTAGTGGAGCTGCAGCCCCGACCGCGGGGAGGACGCCATCGCCGCTGCTTCCT  
CATCAACTGCCTCTACGAGCAGAACTTCGTGTGCAAGTTCGCGCCCAGGGAGGGCTTCAT  
CAACTACCTCACGAGGGAAGTGTACCGCTCCTACCGCCAGCTGCGGACCCAGGGCTTTGG  
AGGGTCTGGGATCCCCAAGGCCTGGGCAGGCATAGACTTGAAGGTACAACCCAGGAACC  
CCTGGTGTGTAAGGATGTGGAACACACAGATTGGCGCCTACTGCGGGGTGACACGGATGT  
CAGGGTAGAGAGGAAAGACCCAAACCAGGTGGAAGTGTGGGGACTCAAGGAAGGCACCTA  
CCTGTTCCAGCTGACAGTGACTAGCTCAGACCACCCAGAGGACACGGCCAAAGTACAGT  
CACTGTGCTGTCCACCAAGCAGACAGAAGACTACTGCCTCGCATCCAACAAGGTGGGTG  
CTGCCGGGGCTCTTTCCACGCTGGTACTATGACCCACGGAGCAGATCTGCAAGAGTTT  
CGTTTATGGAGCTGCTTGGGCAACAAGAACAACCTACCTTCGGGAAGAAGAGTGCAATTCT  
AGCCTGTGCGGGTGTGCAAGGTGGGCCTTTGAGAGGCAGCTCTGGGGCTCAGGCGACTTT  
CCCCAGGGCCCCCTCCATGGAAAGGCGCCATCCAGTGTGCTCTGGCACCTGTCAGCCCAC  
CCAGTTCCGCTGCAGCAATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCC  
CAACTGCCCCGACGCCTCCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGA  
GCTCCAGCGCATCCATTTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACACAGG  
ACTCTGCAAGGAGAGCATCCCGCGCTGGTACTACAACCCCTTCAGCGAACACTGCGCCCG  
CTTTACCTATGGTGGTTGTTATGGCAACAAGAACAACCTTTGAGGAAGAGCAGCAGTGCCT  
CGAGTCTTGTGCGGGCATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCAT  
TCCCAGCACAGGCTCTGTGGAGATGGCTGTACAGTGTTCCTGGTCATCTGCATTGTGGT  
GGTGGTAGCCATCTTGGGTACTGCTTCTTCAAGAACCAGAGAAAGGACTTCACGGACA  
CCACCACCACCCACCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGA  
GCACCTGGTCTATAACCACACCACCCGGCCCCCTCTGAGCCTGGGTCTCACCGGCTCTCAC  
CTGGCCCTGCTTCCTGCTTGCCAAGGCAGAGGCCTGGGCTGGGAAAAAATTTGGAACCAG  
ACTCTTGCCCTGTTTCCCAGGCCCACTGTGCCTCAGAGACCAGGGCTCCAGCCCCCTCTTG  
AGAAGTCTCAGCTAAGCTCACGTCTTGAGAAAGCTCAAAGGTTTGGGAAGGAGCAGAAAAC  
CCTTGGGCCAGAAGTACCAGACTAGATGGACCTGCCTGCATAGGAGTTTGGAGGAAGTTG  
GAGTTTTGTTTCTCTGTTCAAAGCTGCCTGTCCCTACCCCATGGTGTCTAGGAAGAGGAG  
TGGGGTGGTGTGAGACCCTGGAGGCCCCAACCCCTGTCTCTCCGAGCTCCTCTTCCATGCT  
GTGCGCCAGGGCTGGGAGGAAGGACTTCCCTGTGTAGTTTGTGCTGTAAAGAGTTGCTT  
TTTGTTTATTTAATGCTGTGGCATGGGTGAAGAGGAGGGGAAGAGGCCTGTTTGGCCTCT  
CTGTCTCTCTTCTCTTCCCCCAAGATTGAGCTCTCTGCCCTTGATCAGCCCCACCCCA  
GCCTAGACCAGCAGACAGAGCCAGGAGAGGCTCAGCTGCATTCGCGAGCCCCCACCCTG  
AGGTTCTCCAACATCACAGCCCAGCCCACCCACTGGGTAATAAAAGTGGTTTGTGGAAAA  
AAAAAAAAAAAAAAAAAAAAA



CCCACGCGTCCGCACCTTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTTCGGGTCA  
 ACATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGGATTTCAGGCTCGCCAGCGCCC  
 AGCCAGGGAGCCGGCCGGGAAGCGCGATCGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGC  
 TCCTGCTGTTTCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCC  
 AGCCCTGGACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAG  
 TGAAAGATCACGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACT  
 TTGGGGAGAAGAGAGCCCTTCGAGATAATCGAATTTCAGCTGGTTACCTCTACGCCCCACG  
 AGCTCAGCATCAGCATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAA  
 TCTTCACTATGCCTGTGCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGA  
 AGCCCATCATCACTGGTTATAAATCTTCATTACGGGAAAAGACACAGCCACCCTAAACT  
 GTCAGTCTTCTGGGAGCAAGCCTGCAGCCCCGGCTCACCTGGAGAAAAGGGTGACCAAGAAC  
 TCCACGGAGAACCAACCCGCATACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCA  
 GCTCGGTGACATTCCAGGTTACCCGGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGA  
 ACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTCAACGCATTGAAGTTTTATACA  
 CACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTGAGGGGCCAGAAGCTGTTGC  
 TACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTATGGGAGAAGGAGGGCA  
 GTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTTTCCTCAACAAGA  
 GTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACAAGGCCTACT  
 ACACCCTCAATGTTAATGACCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACCACGCCA  
 TCATCGGTGGGATCGTGGCTTTTCAATTGTCTTCTGCTGCTCATGCTCATCTTCTCTTG  
 GCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG  
 ATGCTCCAGACGCGGACACGGCCATCATCAATGCGAGAAGGCGGGCAGTCAGGAGGGGACG  
 ACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCACTTTCCTGCGCCCCCCCAGGGGCCCT  
 GTGGGGAGTCTGGGGCCGTACCAACCCCGGACTTGTACAGAGCAACCGCAGGGGCCGCC  
 CTCCCGCTTGCTCCCCAGCCCCACCCACCCCCCTGTACAGAATGTCTGCTTTGGGTGCGGT  
 TTTGTACTCGGTTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGGTTGCCCTCAG  
 CCCTTTCCGTGGCTTCTCTGCATTTGGGTATTATTATTTTTGTAACAATCCCAAATCAA  
 ATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAA  
 AAACA





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## FIGURE 45

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGG  
 AGGACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATT  
 TTACCATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCA  
 TCCAGTCATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTG  
 TATTTTATTTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGG  
 CTTTTTCTCTGAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAAC  
 TCCTGGCCTGCCCTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAA  
 GCTTGACCTCAGTGCCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACA  
 ACCAAATTAATAATGCTGGATTTCTCTGCAGAACTGCACAATGTACAGTCGGTGCACACGG  
 TCTACCTGTATGGCAACCAACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTCAGAG  
 TTCTCCATTTGCAGGAAAACAATATTCAGACCATTTCACGGGCTGCTCTTGCCCAGCTCT  
 TGAAGCTTGAAGAGCTGCACCTGGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACG  
 GGGCCTTCCGGGAGGCTATTAGCCTCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCA  
 GTGTGCCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGGATGAAAATCGAATTG  
 CTGTCATATCCGACATGGCCTTCCAGAATCTCACGAGCTTGGAGCGTCTTATTGTGGACG  
 GGAACCTCCTGACCAACAAGGGTATCGCCGAGGGCACCTTCAGCCATCTCACCAAGCTCA  
 AGGAATTTTCAATTGTACGTAATTGCTGTCCCACCCTCCTCCCGATCTCCAGGTACGC  
 ATCTGATCAGGCTCTATTTGCAGGACAACCAGATAAACCACATTCTTTTGACAGCCTTCT  
 CAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAACTGCGGATGCTGATC  
 AAGGGGTTTTTGATAATCTCTCCAACCTCAAGCAGCTCACTGCTCGGAATAACCCTTGGT  
 TTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAAATATATCCCTTCATCTCTCA  
 ATTGTGCGGGGTTTTCATGTGCCAAGGTCTGAACAAGTCCGGGGGATGGCCGTCAGGGAAT  
 TAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTGCCTCTCTTACCCCAG  
 CCCCAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTATTCCAAACCCTAGCA  
 GAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTCCTGACTGGGATG  
 GCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGA  
 ATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATACAAACCTCA  
 CATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAGTCAGCG  
 GTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATTTGTT  
 TAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTACAGAGCCA  
 CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
 CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATAT  
 TTGTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACA  
 CCTCCCAGAAGTGGAAATACAACCGGGGGCGGGCGGAAAGATGATTATTGCGAGGCAGGCA  
 CCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAA  
 ATAACGATCAACTCCTTAAAGGAGATTTTCACTGTCAGCCCATTTACACCCCAAATGGGG  
 GCATTAATTACACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGC  
 CAGACCTGGAGCACTGCCATACGTGACAGCCAGAGGGCCAGCGTTATCAAGGCGGACAAT  
 TAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAA  
 TGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA  
 TGGGATTTAAAAAAGTGCTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAA  
 TCTTTGCTTTTTTAAATCTT

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## FIGURE 46

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLG  
IPEGVTVLVYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENN  
IQTISRALAQLLKLEELHLDNNSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPV  
DLQELRVNENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRN  
SLSHPPPDLPGLHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLS  
NLKQLTARNNPWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELNMNLLSC  
PTTTPGLPLFTPAPSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPP  
ISERIQLSIHFNVDTSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSL  
VNLEPRSTYRICLVPLDAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSP  
FLLAGLIGGAVIFVLVLLSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSIL  
EMTETSFQIVSLNNDQLLKGDFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**  
amino acids 1-42

**Transmembrane domain:**  
amino acids 542-561

**N-glycosylation site:**  
amino acids 202-206, 298-302, 433-437, 521-525, 635-639,  
649-653

**Casein kinase II phosphorylation site:**  
amino acids 204-208, 407-411, 527-531, 593-597, 598-602,  
651-655

**Tyrosine kinase phosphorylation site:**  
amino acids 319-328

**N-myristoylation site:**  
amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site:**  
amino acids 581-585

**Leucine zipper pattern:**  
amino acids 164-186

**Phospholipase A2 aspartic acid active site:**  
amino acids 39-50

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## FIGURE 47

GCAGCGAGCGCCGGGTGCGGCCCTGCCGCCGCAGGGATGTGACCTTCACCGTCGCTTAGC  
CAGGATGACCGGAGCCCCGTGTCTCGCGGCGTCCGCGCCTCGCTTCAGCCTCCCGGGTGCT  
CTGACCGCACGCTCCCGGCTGCTAGGCTCCCCGGCACCGGCCCTCGCCATGCGGCCACCGC  
CCGGCCCCCGCCCGCCCTGGGCACTGCGCTTCTGCTGCTCCTGCTGGCTTCCGAGTCTT  
CTCACACTGTGCTGTTGCGGGCGCGTGAGGCGGCGCAGTTTCTGCGGCCAGGCAGCGCC  
GCGCCTACCAAGTCTTTCGAGGAGGCCAAGCAGGGCCACCTGGAACGGGAGTGCGTGAGG  
AGGTGTGCAGCAAAGAGGAGGCCAGAGAGGTGTTTCGAGAACGACCCCGAGACGGAGTATT  
TCTATCCACGATATCAAGAGTGCATGAGAAAAATATGGCAGGCCTGAAGAAAAAAACCCAG  
ATTTTCGCCAAATGTGTTTCAAGAACTTGCCCTGACCAGTGCACCCCAAACCTTGTGATAAGA  
AGGGTACTCATATCTGCCAAGACCTCATGGGCAACTTCTTCTGCGTGTGCACAGATGGCT  
GGGGAGGCCGGCTCTGTGACAAAGATGTCAATGAGTGTGTCCAGAAGAATGGGGGCTGCA  
GCCAGGTCTGCCACAACAAACCAGGAAGCTTCCAATGTGCCTGCCATAGTGGCTTCTCGC  
TTGCATCAGACGGCCAGACCTGCCAAGATATCGATGAATGCACAGACTCAGACACCTGTG  
GGGACGCGCGATGCAAGAACTTGCCAGGCTCCTACTCTTGCCTCTGCGATGAGGGATATA  
CATAAGCTCCAAGGAGAAGACCTGCCAAGATGTGGACGAGTGCCAGCAGGATCGCTGTG  
AGCAGACCTGTGTCAACTCCCCAGGCAGCTATACCTGCCACTGTGATGGGCGAGGGGGCC  
TAAACTATCCCCAGACATGGATACTTGTGAGGACATCTTACCATGTGTGCCCTTCAGCA  
TGGCCAAGAGCGTGAAGTCCTTGTACCTGGGCCGCATGTTACGCGGGACCCCGTGATTA  
GACTACGCTTCAAGAGGCTTCAGCCTACCAGGCTGCTGGCTGAATTTGACTTCCGCACTT  
TTGACCCTGAAGGAGTCTTCTTCTCGCTGGAGGCCGTTTCAGACAGCACCTGGATTGTCC  
TGGGCCCTAAGAGCTGGGCGGCTTGAGCTGCAGCTTCGGTACAATGGCGTTGGGCGCATCA  
CCAGCAGCGGGCCAACCATCAACCACGGCATGTGGCAAACCTATCTCCGTGGAAGAGCTGG  
AACGTAACCTTGTTCATCAAGGTCAACAAAGATGCTGTAATGAAGATCGCGGTAGCTGGGG  
AGCTGTTTTAGCTGGAGAGGGGCCCTCTATCACCTGAATCTCACCGTGGGCGGCATTCCCT  
TCAAGGAGAGTGAGCTCGTCCAGCCGATTAACCCTCGCCTGGATGGGTGCATGAGGAGTT  
GGAAGTGGCTGAACGGGGAAGACAGCGCCATCCAGGAGACAGTCAAGGCAAACACAAAAA  
TGCAGTGCTTCTCTGTGACAGAAAGGGGCTCCTTCTTCCCGGGGAATGGATTTGCTACCT  
ACAGGCTCAACTACACCCGAACATCGCTGGATGTGCGCACGGAAACCACTGGGAAGTTA  
AAGTTGTGGCTCGGATCCGCCCTGCCACGGACACGGGGGTGCTGCTGGCGCTGGTGGGGG  
ACGACGATGTCGTCTCTGTGGCCCTAGTCGACTACCACTCTACAAAGAAGCTCAAGA  
AGCAGTTGGTGGTCTTGGCAGTTGAGGATGTTGCCCTGGCACTGATGGAAATCAAGGTGT  
GCGACAGCCAGGAACACACGGTCACTGTCTCCCTGCGGGAGGGTGAGGCCACCCTAGAAG  
TGGATGGCACAAAGGGCCAGAGTGAAGTGAGCACTGCCAGCTGCAGGAGCGACTGGACA  
CACTTAAGACACATCTGCAAGGCTCTGTGCACACCTATGTTGGAGGCCTGCCAGAAGTAT  
CGGTGATTTCTGCACCCGTCCTGCGTTCCTACCGCGGATGCATGACTCTGGAGGTAAACG  
GGAAAATCCTGGACCTGGATACGGCCTCGTACAAGCACAGTGACATCACCTCCCACTCCT  
GCCCCCTGTGGAGCATGCCACCCCCCTAGACCGAGCTGCAAGAGGGCTCCACACCTAAAG  
ACAAAAATGAAGCAGGGTTTGGACACACAGCACTGGCTCCTCTCGCATGGTCTTGCCTTG  
CTGGAGCAGCGTGGACCGCCCTTGTGGTTTTTTTTTCTTGAGATCTTCTTTTTTGCCTTG  
TAACATATCTGTACATAATGGACGGGTGTGCGGTACCGGCTGCTCAGAGAGAGCCACGT  
GACCTGGTGGGAGCTGGCTGGAAGGGGCTGGGCTAGAGGGGCTGGCAGTTTGCAGCAGAA  
CGGATGTGAAGAAAATAATTCTCTATTATTTTATTACTACATGCTTCTTCTGACTCTA  
AAATATGGAATAAAATATTTACAGAAACCTTTTTTAAAAA

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## FIGURE 48

MPPPPGPAAALGTALLLLLLLASESSHTVLLRAREAAQFLRPRQRRAYQVFEEAKQGHLE  
ECVEEVCSKEEAREVFENDPETEYFYPRYQECMRKYGRPEEKNPDFAKCVQNLDPDQCTPN  
PCDKKGTHICQDLMGNFFCVCTDGGWGGRLCDKDVNECVQKNGGCSQVCHNKPGSFQCACH  
SGFSLASDGQTCQDIDECTDSDTCGDARCKNLPGSYSCLCDEGYTYSSKEKTCQDVDECQ  
QDRCEQTCVNSPGSYTCHCDGRGGLKLSPDMDTCEDILPCVPFSSMAKSVKSLYLGRMFSG  
TPVIRLRFKRLQPTRLLAEFDFTFDPEGVLFFAGGRSDSTWIVLGLRAGRLELQLRYNG  
VGRITSSGPTINHG MWQTISVEELERNLVIKVNKDAVMKIAVAGELFQLERGLYHLNLT  
GGIPFKESELVQPINPRLDGCMRSWNWLNGEDSAIQETVKANTKMQCFSVTERGSFFPGN  
GFATYRLNYTRTSLDVGTETTWEVKVVARIRPATDTGVLLALVGDDDVVISVALVDYHST  
KKLKKQLVVLAVEDVALALMEIKVCDSQEHTVTVSLREGEATLEVDGPKGQSEVSTAQLQ  
ERLDTLTKTHLQGSVHTYVGGLEPVSVISAPVTAFYRGCMTLEVNGKILDLDLTASYKHSDI  
TSHSCPPVEHATP

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## FIGURE 49

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGC  
CCGGCGGCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCA  
GTCGGGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGT  
GCCTGCTGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGG  
CTCCAGTCAAGCCCGGCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGA  
TGTTCCGCGAGGTTGAGGAAGCTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGG  
AAGAGATGGAGGCAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCT  
TACCTCCCAGCTATCACAAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCC  
ATGTGCACCCGAGAAATTCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAG  
AGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCG  
ACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGC  
CATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGT  
GTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGCTGTTCCCTG  
TGTGCACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGG  
ACCTCATCACCTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTG  
GCCTCCTCTGCCAGCCCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTTCGTGG  
GGAGCCGTGACCAAGATGGGGAGATCCTGCTGCCCAGAGAGGTCCCCGATGAGTATGAAG  
TTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTG  
AAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCTGCACTGCTGGGAGGGGAAGAGA  
TTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCCA  
GGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACATCTTCTTCCAGTAAGTT  
TCCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCCAGCTCCCCCAGGCTGTTCT  
CCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAACTGCAGGAGCAGTTT  
GCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCGTTTGT  
TCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAA  
AAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTT  
CAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTTCATCCAGCA  
GTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCC  
TCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTC  
ATCTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACACCAGCCTTGGTGCCA  
CCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGA  
ATTAAGGTCAAACAACTAATTCTCACATCCCTCTAAAAGTAAACTACTGTTAGGAACAGCAGT  
GTTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCT  
CTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTAA  
CCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAAT  
CACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAA  
TGATGTTTTTCAGGTGTCATGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTT  
TAAAGTTGCACATGATTGTATAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACAT  
AAGTTGCATTTAGAAATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAA  
AAAAAA

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## FIGURE 50

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMED  
TQHKLRSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITN  
NQTGQMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMMLCTR  
DSECCGDQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGEL  
CHDPASRLLDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILL  
PREVPDEYEVGSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site:**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site:**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site:**

amino acids 202-208, 217-223

**Amidation site:**

amino acids 140-144

## FIGURE 51

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCC  
GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT  
GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC  
TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC  
CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG  
GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC  
AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT  
GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC  
TTCAGTTG<sup>CC</sup>ACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA  
GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC  
AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTCCGGTG  
CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG  
GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC  
ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTC  
TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA  
CAGAGCCACCTAGTTTGTCTTTGTTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA  
AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCC  
TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC  
ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG  
CTGGATCTCATCGTAGATACCATGGGTTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA  
GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCTAAATCTTTG  
GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTTCTACTGGATTCTGAAAGCT  
GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT  
CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT  
GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT  
GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT  
TGGAATTTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG  
ATCAAAATAAAGGATGATAATAGATATTAA

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## FIGURE 52

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN  
SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT  
GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL  
YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA  
VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH  
VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG  
INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS YKN  
LAFYWILKAGHMVPSDQGDMA LKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site:**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 101-105

**Casein kinase II phosphorylation site:**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site:**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175, 187-193, 195-201, 331-337, 332-338, 360-366



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## FIGURE 53

GTCTGTTCCCAGGAGTCCTTCGGCGGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACA  
AAGGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCC  
CTGGCATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAAT  
AATCCTGTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAG  
TTTGACCAAGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTAT  
GAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGAC  
ACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAG  
GTCAAGCTCATCGTGCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCC  
ACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAA  
TACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTC  
AGCAACTCTTCCTATGTCTGAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCA  
GCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACACCCATGACT  
TCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGGTGATCGTGGCAGCCGTC  
CTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGA  
GGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAGGTGATTTACAGCCAGCCT  
AGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTGGTGTGAGCCTGGTGC  
GCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACTCTGGCCCCCTGAT  
GTCTGTAGTTTACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCCCCTACTTCT  
TCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTCCCTCCC  
TTTCCTACCACTGCTGAGTGGCCTGGAACCTGTTTTAAAGTGTTTATTCCTCATTTCTTTG  
AGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA  
TGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCCACCTGGCTGGCAGGGATCTTTGAAT  
AGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGT  
TCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGG  
TCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCC  
CTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGG  
AGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAGGATTTAAA  
ACCGCTGCTCTAAAGAAAAGAAAAGTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCC  
CAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTTCGGGATCAGCCTGACCAACAT  
GGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCC  
AGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## FIGURE 54

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRV  
EWKFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYG  
EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGI VMPTNPKST  
RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV  
AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**  
amino acids 1-27

**Transmembrane domain:**  
amino acids 238-255

**N-glycosylation site:**  
amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**  
amino acids 270-274

**Casein kinase II phosphorylation site:**  
amino acids 34-38, 82-86, 100-104, 118-122, 152-156,  
154-158, 193-197, 203-207, 287-291

**N-myristoylation site:**  
amino acids 105-111, 116-122, 158-164, 219-225, 237-243,  
256-262

GTTGTGTCTCCTTCAGCAAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACAC  
 AATCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAG  
 AAGAAAAAAATC**AT**GAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAAT  
 CTTACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGC  
 CACCTTCCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAG  
 GTGCACTATTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTA  
 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAAC  
 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC  
 GGTGCAGACAGACAACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC  
 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC  
 CTGCATAGCAACTGGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGC  
 GGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC  
 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAA  
 GGTACCGTGAACCTATCCACCATACATTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGG  
 ACAAAGGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTCAGCAGAATTCAGTGGTA  
 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTT  
 CCTCTCAAACTCATCTTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGCGT  
 GGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCCGT  
 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCCTCTTCT  
 GGTCTTGACCTGCTTCTCAAATTT**TGA**TGTGAGTGCCACTTCCCCACCCGGGAAAGGCT  
 GCCGCCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA  
 TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAC  
 AAAGAATACTTTGGGGGAAAGAGTTTAAAAAAGAAATTGAAAATTGCCTTGAGATA  
 TTTAGGTACAATTGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGA  
 CCACTGCAAGCTGCATCTGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTC  
 TCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCATCA  
 GTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTG  
 GTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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## FIGURE 56

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTID  
NRVTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTD  
NHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFV  
SEDEYLEIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYI SEAKGTGV PVGQKGT  
LQCEASAVPSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGN YTCVASNK  
LGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLLKF

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## FIGURE 57

GCTGCGCCGGCTGCGGCTGCAGGGGAATCCGCTGTGGTGCGGCTGCCAGGCGCGGCCCT  
 ACTCGAGTGGCTGGCGCGGGCGCGCGTGCCTCGGACGGCGCGTGCCAGGGGGCCGCGGCG  
 CCTGCGGGGCGAGGCTCTGGACGCCCTGCGGCCCTGGGACCTGCGCTGCCCTGGGGACGC  
 GGCGCAGGAAGAGGAAGAGCTGGAAGAGCGGGCTGTGGCCGGGCCCCGCGCCCCCTCCGCG  
 CGGCCCTCCGCGCGGGCCCCGGGGAGGAGCGGGCAGTCGCGCCTTGCCCTCGCGCCTGCGT  
 GTGCGTCCCCGAGTCCCGGCACAGCAGCTGCGAGGGCTGCGGCCTGCAGGCGGTGCCCCG  
 CGGCTTCCCCAGCGACACCCAGCTCCTGGACCTGAGGCGGAACCACTTCCCCCTCGGTGCC  
 CCGAGCGGCCTTCCCCGGNCTGGGCCACCTGGTGTGCTGCACCTGCAGCACTGCGGCAT  
 CGCGGAGCTGGAAGCGGGCGCCCTGGCCGGGCTGGGCCGCCTGATCTACCTGTACCTCTC  
 CGACAACCAGCTCGCAGGCCTCAGCGCTGCTGCCCTTGAAGGGGCTCCCCGCCTCGGCTA  
 CCTGTACCTAGAACGCAACCGTTTCCTGCAGGTGCCAGGGGCTGCCNTGCGCGCCCTGCC  
 CAGCCTCTTCTCCCTGCACCTGCAGGACAACGCTGTGGACCGCCTGGCACCTGGGGACCT  
 GGGGAGAACACGGGCCTTGCGCTGGGTCTACCTGAGTGGAAACCGCATCACCGAAGTGT  
 CCTTGGGGCGCTGGGCCAGCTCGGGAGCTGGAGAAGCTGCACCTGGACAGGAATCAGCT  
 GCGAGAGGTGCCCCTGGGGCCTTGAGGGGCTGCCCTCCTGGAGCTGCAGCTCTC  
 GGGCAACCCACTCAGGGCCTTGCGTGACGGAGCCTTCCAGCCTGTGGGCAGGTGCTGCA  
 GCACCTCTTCTGAAACAGCAGTGGCCTGGAGCAGATTTGTCTTGGGGCCTTTTCAGGCCT  
 GGGGCCCGGGCTCCAGAGCCTGCACCTGCAGAAGAACCAGCTTCCGGGCCCTGCCTGCCCT  
 GCCAGTCTCAGCCAGCTGGAGCTCATCGACCTCAGCAGCAATCCCTTCCCCCTGTGACTG  
 CCAGCTGCTTCCGCTGCACAGGTGGCTTACTGGGCTGAACCTGCGGGTGGGGGCCACCTG  
 CGCCACCCCTCCCAATGCCCGTGGCCAGAGGGTGAAGGCTGCAGCTGCTGTCTTTGAAGA  
 CTGCCCCGGGCTGGGCTGCCAGAAAGGCCAAGCGGACACCAGCCTCCAGGCCAGTGCCAG  
 GAGAACCCCCATCAAAGGAAGACAGTGTGGAGCAGATAAGAACATCCTCTTCCCCACATG  
 GTACCACACTGTGGAGCCCACCTCGCTGTCATAGGCCTGCGGCTCTGAAGGATGGCTTTG  
 CCCGCTCCCGCTCTGCCCCCTCAAGTGGAACCCAAGCTGGGCTCAGAATCTGTAGAGTGAG  
 GCCCCACCAAGGGAAACGACACCCACGGCCTGAGAGCCAGGTGGAGTCTTGCCACTCAGC  
 TGCCTGCCTTTGCTCCCACCCTCTCCACCCTCAAAGAGGTCTCGAGGGGACACTCTGAA  
 GGCACCTGGCTCAGAACCACTGCCATCCAAGGAGCGAGGAGTCCAGGGGCTGAGCAAATG  
 CAGCGGGGAGGTGGCAGTTCCCCTGCTTCCCGATCCTCATTTTCTGCTTCACTTGACTC  
 CTCCAGATAGGAGCTGCTCTCACTGCCACACTGCTG

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## FIGURE 58

LRRLRLQGNPLWCGCQARPLLEWLARARVRSDGACQGPRRLRGEALDALRPWDLRCPGDA  
AQEEEELEERAVAGPRAPPRGPPRGPEERAVAPCPRACVCPESRHSSCEGCGLQAVPR  
GFPSDTQLLDLRRNHFPSPRAAFPGLGHLVSLHLQHCGIAELEAGALAGLGRLIYLYLS  
DNQLAGLSAAALEGAPRLGYLYLERNRFLQVPGAAXRALPSLFSHLQDNAVDR LAPGDL  
GRTRALRWVYLSGNRITEVSLGALGPARELEKLHLDRNQLREVPTGALEGLPALLELQLS  
GNPLRALRDGAFQPVGRSLQHLFLNSSGLEQICPGAFSGLGPGLQSLHLQKNQLRALPAL  
PSLSQLELIDLSSNPFPCDCQLLPLHRWLTGLNLRVGATCATPPNARGQRVKAAAVFED  
CPGWAARKAKRTPASRPSARRTPIKGRQCGADKNILFPTWYHTVEPTSLS

**Signal sequence:**

None

**Transmembrane domain:**

None

**N-glycosylation site:**

325-328

**Glycosaminoglycan attachment site:**

338-341

**Protein kinase C phosphorylation site:**

438-440

**N-myristoylation site:**

166-171, 186-191, 253-258, 286-291, 335-340, 339-344, 450-455

**Leucine rich repeat N-terminal domain:**

94-123

**Leucine Rich Repeat:**

125-148, 149-172, 173-196, 197-220, 221-244, 245-268, 269-292, 293-316, 318-341, 343-364, 365-386

**Leucine rich repeat C-terminal domain:**

374-422

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## FIGURE 59

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTG  
CTCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACT  
GTGTCCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGG  
AAGGGTGGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAG  
GAGACAATGAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTG  
ACCCTGTGGAACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGG  
GGCCCCGATGAGTCTTTACTGATCTCTCTGTTCTTTCCAGGACCCTGCTGTCCTCCC  
TCCCCTTCTCCACCTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCT  
CAGCAAACCCAGCCCCCAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCC  
AAGCAGGGGAAGACAGGGGCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCAC  
GAAAGGACTTCTCAGTACACAGGAACCTCTCCTCACCCAGCGACCTCTCCTCTGCAGGG  
AGTCCCGCCCCCATGTCAGCTGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTC  
AGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTC  
CTGGTGTCTGAGCCTTCTGTGTCAGCCGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTC  
CTGTGAGAAAGGAAGCTCAACAGGGCCACGGAGACACAGAGGAACGAGAAGTTCTGGCTC  
TCACGCTTGACTGCGGAGGAAAAGGAAGCCCTTCCCAGGCCCTGAGGGGGACGTGATC  
TCGATGCCTCCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAGTTTGTCTCAGCG  
TAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGCTGGATCAGC  
ACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCGGACTCCAGGGCT  
CTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCAGCCTGACCTAGAAGCGTTTGTCT  
AGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGAGACTGGGACATCCCTGAT  
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCT  
CAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGCCTCATGCCCAGTGTCTG  
GACCCTGCCTTCCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCCTGGCGTCTCAGAC  
TLAGTCCACGGTCTCCTGCATCAGCTGGTGTGAAGAGGAGCATGCTGGGGTGAGACTG  
GGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAAACG  
TGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGA  
ATTCTAACAATGCCCAGTGACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTGATGAAC  
GCTCACACCCCTTCCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCCAAT  
AGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTC  
CAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
TTGCCTTTNCCATTGCCCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAA  
GAAAACCTTGGCTCCTTCCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTA  
GAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACA  
GGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTCGGGGGTGGTG  
GTAAAGTAGCACAACTACTATTTTTTTTCTTTTTTCCATTATTATTGTTTTTTAAGACAGA  
ATCTCGTGCTGCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCTCCTGG  
GTTCAAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACC  
ACACCTGGCTAATTTTTTGTACTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTG  
GTCTTGAACCTCTGACCTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTA  
CAGGCATGAGCCACTGTGTCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTC  
AGTATGCAAACTTGGAAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA  
TAGTCTCACCAGAGACTATCATTATTTCTTTTGTGTACTTCTTCCACTCTTTTCTTC  
TTCACATAATTTGCCGGTGTTCTTTTTTACAGAGCAATTATCTTGTATATACAACTTTGTA  
TCCTGCCTTTTCCACCTTATCGTTCCATCACTTTATTCAGCACTTCTCTGTGTTTTACA  
GACCTTTTTTATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

amino acids 13-128



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## FIGURE 61

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGAT  
 GGTGAGGTTTGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGAC  
 ATGGAGAACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCC  
 ATCAACCCACACAACCTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGC  
 ATATCTGATGTCAGGAGGACTTTCTGTTTGTGTGTCACCTTTGACCTCTTATTCGTAACA  
 TTACTGTGGATAATAGAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAG  
 GTGATGCAGTATGACTACTATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTTCGA  
 TTTAAAGTGTTAATACTTGCATATGCTGTGTGCAGACTGCGCCATTGGTGCGCAATAGCG  
 TTGACAACGGCAGTGACCAGTGCCTTTTTTACTAGCAAAAGTGATCCTTTTCGAAGCTTTTC  
 TCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTCATCCTTGCCTGGATTGAG  
 ACGTGGTTCTTGGAATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAACAGACTCCTG  
 ATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATGGTCAG  
 TTTTATTTCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
 GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTAAATGTGAAAAACCCCTCACAGA  
 AAGTCATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAA  
 TGGTGACGTCCACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACC  
 TCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCCTGCCCTGGCTGGTAAGGTAA  
 TGTTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAG  
 AAAGTCTTGTGCTGTATTCCTAATCAAAAGACTTAATATATTGAAGTAACACTTTTTTTAG  
 TAAGCAAGATACCTTTTTTATTTCAATTCACAGAATGGAATTTTTTTTGTTCATGTCTCAG  
 ATTTATTTTTGTATTTCTTTTTTAACTCTACATTTCCCTTGTTTTTTAACTCATGCACA  
 TGTGCTCTTTGTACAGTTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTT  
 TTATTTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAA  
 GAAAGGAATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTTTTTATCATGAA  
 ATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAA  
 ATGACTTAAACCATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAAATGAA  
 CTAAATTAAAAA

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## FIGURE 62

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  
FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRL  
RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQA  
EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites:**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

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## FIGURE 63

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCAC  
 ATGGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCCGAGCTCGCCCGAGGTCCGT  
 CGGAGGCGCCCGGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCG  
 GGGATCGGGATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTG  
 GGGACTCACACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTTGCCCTGCCACCAT  
 CAACTGGGGCTTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAA  
 GGGAAACCAAAAAGTGGTGATCACTTACTCCAGTCGTCATGTCTACAATACTTGACTGAG  
 GAACAGAAGGGCCGAGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGAG  
 ATTGAACCTCTGAAGCCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGG  
 CGCTACGTGTGGAGCCATGTCTATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGT  
 GAGTTGGAAGGAGAGCTGACAGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCT  
 GGCACAGAGCCCATTTGTGTATTACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAA  
 CGTCTGCCTCCCAAATCTAGGATTGACTACAACCACCCTGGACGAGTTCTGCTGCAGAAT  
 CTTACCATGTCCTACTCTGGACTGTACCAGTGACAGCAGGCAACGAAGCTGGGAAGGAA  
 AGCTGTGTGGTGCGAGTAACTGTACAGTATGTACAAAGCATCGGCATGGTTGCAGGAGCA  
 GTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCCTCTTGGTGTGGCTGCTAATCCGA  
 AGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATTCGAGAAGATGCT  
 GAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCCTCCTCAGGCTCTCGGAGCTCA  
 CGCTCTGGTTCTTCTCCACTCGCTCCACGACCAATAGTGCCTCACGCAGCCAGCGGACA  
 CTGTCAACTGACGCAGCACCCCGAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTGGGG  
 CCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA  
 ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCTGAATTACAATG  
 GACTTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGC  
 TCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCAGTGAGCATTGCACG  
 GAACAGATTGAGATGAGCATTCTTCTTATACAATACCAAACAAGCAAAAGGATGTAAGCT  
 GATTCTCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAG  
 TCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTGAGGTGAAT  
 ATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAATTTTCAAG  
 AGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACTTATTGGATTATTA  
 GTTATTGAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG  
 AGCTAACCCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
 TTCATTTGTCATAAGGTTTGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA  
 GAAGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAA  
 TAACTATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCAT  
 GATGTTATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTC  
 CCTCAAATCAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACA  
 ACATGTCATTTATCAACGTCCTTAGAAAGAATTTCTTCTAGAGAAAAGGGATCTAGGAAT  
 GCTGAAAGATTACCAACATAACATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAG  
 AATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAA  
 GGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCA  
 GTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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## FIGURE 64

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQ  
KVVITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYV  
WSHVILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLP  
PKSRIDYNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTG  
IVAGALLIFLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSG  
SSSTRSTANSASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTP  
SMIPSQSRAFQTV

**Signal sequence:**  
amino acids 1-16

**Transmembrane domain:**  
amino acids 232-251

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FIGURE 67

CGCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCT  
TCGCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCAC  
CCCTGTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTC  
CAGTCCCCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCT  
ACAGTTACTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACC  
TACTTATGGGAGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACT  
ATGTAACCTGGGAATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTG  
GACCGATGACAAAGTTTATTTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCT  
ATGACGACGGAAGCACAAAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGA  
GTAAAGAAATCAGGAACATGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCT  
TGGAACCTCCCTCCGAAATTCAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACA  
GATATTCTGGCTGGCCTGCAGAGATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCT  
GACACTGCAGGGTCCTGAGTAAATGTGTTCTGTATAAAACAAATGCAGCTGGAATCGCTCA  
AGAATCTTATTTTTTCTAAATCCAACAGCCCATATTTGATGAGTATTTTTGGGTTTGTGTA  
AACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCAGTATTTTTTATACCAGTAT  
TTTATGTAGTGAAGATGTCAATTAGCAGGAAACTAAAATGAATGGAAATTCTTAAAAAAA  
AAA

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## FIGURE 68

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKR  
QKCDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGN  
VTATRCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIR  
NMKFRSSWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

**Signal sequence:**

amino acids 1-20

**N-glycosylation sites:**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site:**

amino acids 80-84

**N-myristoylation sites:**

amino acids 81-87, 108-114, 119-125



ACACAACCTTTACACCTGAATGAACGCCAAACCTCTATGGATATATAAAGGGAAGCTTGAG  
GAGGAATTTTCACAGTTACAGTGCAGAAGCAGAAGCAAAAGAATTAACCAGCTCTTCAGTC  
AAGCAAATCCTCTACTCACCATGCCTTCCTCCTGCCATTTCATTTCTATCTCCTTCCCCTTG  
CATGCATCCTAATGAAAAGCTGTTTGGCTTTTAAAAATGATGCCACAGAAATCCTTTATT  
CACATGTGGTTAAACCTGTTCCAGCACACCCCAGCAGCAACAGCACGTTGAATCAAGCCA  
GAAATGGAGGCAGGCATTTTCAGTAACACTGGACTGGATCGGAACACTCGGGTTCAAGTGG  
GTTGCCCGGGAAGCTGCGTTCCACCAAATACATCTCTGATGGCCAGTGCACCAGCATCAGCC  
CTCTGAAGGAGCTGGTGTGTGCTGGCGAGTGCTTGCCCCTGCCAGTGCTCCCTAACTGGA  
TTGGAGGAGGCTATGGAACAAAGTACTGGAGCAGGAGGAGCTCCCAGGAGTGGCGGTGTG  
TCAATGACAAAACCCGTACCCAGAGAATCCAGCTGCAGTGCCAAGATGGCAGCACACGCA  
CCTACAAAATCACAGTAGTCACTGCCTGCAAGTGCAAGAGGTACACCCGGCAGCACAAACG  
AGTCCAGTCACAACTTTGAGAGCATGTACCTGCCAAGCCAGTCCAGCATCACAGAGAGC  
GGAAAAGAGCCAGCAAATCCAGCAAGCACAGCATGAGTTAGAACTCAGACTCCCATACT  
AGACTTACTAGTAACCATCTGCTTTACAGATTTGATTGCTTGAAGAGACTCAAGCCTGCCA  
CTGCTGTTTTCTCACTTGAAAGTATATGCTTTCTGCTTTGTATCAAACCCAGCAAGCTGTC  
TTAAGTATCAGGAACCTTCTTTGGGAATAGTTTTTTCCTTTTAAAGTTTTTCAAGATGTAGG  
TATATGCATGAATGCAATTTGCATTTAAATTCCACGTATCCCTGTAGTTTTAAATTCCTCA  
TTGGTCTTAAAAGACTGTTGATACTATAAACATCAGTGGAATCAATTATATTTTAAACA  
GAAAAGGGCTT



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## FIGURE 71

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAA  
 AGGCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTC  
 CGAATCAGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGA  
 CCTCGTGCGGCCAAGACGTGGATGTTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACAC  
 TCCAGGGCACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCT  
 TGGCAGGCGGCCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTTAGGTGGC  
 AACTGGGTCCTTACAGCTGCCCCTGTAAAAAACCGAAATACACAGTACGCCTGGGAGAC  
 CACAGCCTACAGAATAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTTCAGTCCATCCCA  
 CACCCCTGCTACAACAGCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAA  
 CTGCGTGACCAGGCATCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGC  
 ACCCAGCCTGGCCAGAAGTGCACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAG  
 AATTTTCCTGACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAG  
 GATGCTTACCCGGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCT  
 GACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGTGATGGTGCCTCCAGGGCATC  
 ACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATC  
 TGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGCTTGATTCTAGGATAAG  
 CACTAGATCTCCCTTAATAAACTCACAACCTCTCTGGTTC



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## FIGURE 73

CTCGGGCGCGCACAGGCAGCTCGGTTTGGCCCTGCGATTGAGCTGCGGGTTCGCGGCCGGCG  
 CCGGCCCTCTCCAATGGCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTCGGCAAAGG  
 CAGTCGAGTGTTTGCAGACCGGGGCGAGTCCTGTGAAAGCAGATAAAAGAAAACATTTAT  
 TAACGTGTCATTACGAGGGGAGCGCCCGGGGCTGTGCGCACTCCCCGCGGAACATTT  
 GGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTCACGTG  
 TTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTAT  
 TAGCGATGCCCCCTGGTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCG  
 CTTCCTCCCTCGTTTCCAGCTCCTGGGCGAATCCACATCTGTTTCAACTCTCCGCCGA  
 GGGCGAGCAGGAGCGAGAGTGTGTGCAATCTGCGAGTGAAGAGGGACGAGGGAAAAGAAA  
 CAAAGCCAACAGACGCAACTTGAGACTCCCGCATCCCAAAGAAGCACCAGATCAGCAAAA  
 AAAGAAGATGGGGCCCCCGAGCCTCGTGCTGTGCTTGCTGTCCGCAACTGTGTTCTCCCT  
 GCTGGGTGGAAGCTCGGCCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGA  
 CCGCAGGAACATCCGCCCAACATCATCTGGTGCTGACGGACGACCAGGATGTGGAGCT  
 GGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATCATGGAGCAGGGCGGGGCGCACTT  
 CATCAACGCCTTCGTGACCACACCCATGTGCTGCCCCTCACGCTCCTCCATCCTCACTGG  
 CAAGTACGTCCACAACCACAACACCTACACCAACAATGAGAAGTGTCTCCTCGCCCTCCTG  
 GCAGGCACAGCACGAGAGCCGCACCTTTGCCGTGTACCTCAATAGCACTGGCTACCGGAC  
 AGCTTTCTTCGGGAAGTATCTTAATGAATACAACGGCTCCTACGTGCCACCCGGCTGGAA  
 GGAGTGGGTTCGACTCCTTAAAACTCCCGCTTTTATAACTACAGCTGTGTGCGAACGG  
 GGTGAAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCACAGACCTCATCACCAA  
 TGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCCTCAT  
 GGTTCATCAGCCATGCAGCCCCCACGGCCCTGAGGATTACGCCCCACAATATTCACGCCT  
 CTTCCCAAACGCATCTCAGCACATCACGCCGAGCTACAACCTACGCGCCCAACCCGGACAA  
 AACTGGATCATGCGCTACACGGGGCCCATGAAGCCCATCCACATGGAATTCACCAACAT  
 GCTCCAGCGGAAGCGCTTGCAGACCCTCATGTGCGGTGGACGACTCCATGGAGACGATTTA  
 CAACATGTCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGCCGACCA  
 CGGTTACCACATCGGCCAGTTTGGCCTGGTGAAAGGGGAAATCCATGCCATATGAGTTTGA  
 CATCAGGGTCCCGTTCTACGTGAGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCCA  
 CATCGTCTCAACATTGACCTGGCCCCCACCATCCTGGACATTGCAGGCCTGGACATACC  
 TGCGGATATGGACGGGAAATCCATCCTCAAGCTGCTGGACACGGAGCGGCCGGTGAATCG  
 GTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGACTCCTTCTTGGTGGAGAGAGGCAA  
 GCTGCTACACAAGAGAGACAATGACAAGGTGGACGCCAGGAGGAGAACTTTCTGCCCAA  
 GTACCAGCGTGTGAAGGACCTGTGTGACGCTGCTGAGTACCAGACGGCGTGTGAGCAGCT  
 GGGACAGAAGTGGCAGTGTGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAA  
 GGGCCCCATGCGGTGGGCGGCAGCAGAGCCCTCTCCAACCTCGTGCCCAAGTACTACGG  
 GCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTCAGCCTGGCCGGACG  
 CCGGAAAAAACTCTTCAAGAAGAAGTACAAGGCCAGCTATGTCCGCAGTCGCTCCATCCG  
 CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCACGTAGGCCTGGGTGATGCCGCCCA  
 GCCCCGAAACCTACCAAGCGGCACTGGCCAGGGGGCCCCCTGAGGACCAAGATGACAAGGA  
 TGGTGGGGACTTCAGTGGCACTGGAGGCCTTCCCGACTACTCAGCCGCCAACCCCATTA  
 AGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCAGTGTGACCTGGACCTGTA  
 CAAGTCCCTGCAGGCCTGGAAAGACCACAAGCTGCACATCGACCACGAGATTGAAACCT  
 GCAGAACAAAATTAAGAACCTGAGGGAAGTCCGAGGTACCTGAAGAAAAAGCGGCCAGA  
 AGAATGTGACTGTCAAAAATCAGCTACCACACCCAGCACAAAGGCCGCCTCAAGCACAG  
 AGGCTCCAGTCTGCATCCTTTAGGAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGTT  
 GCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGCTCAAGCGCCTGCAGAACAAACGA  
 CACGTGCAGCATGCCAGGCCTCACGTGCTTACCCACGACAACCAGCACTGGCAGACGGC

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GCCTTTCTGGACACTGGGGCCTTTCTGTGCCTGCACCAGCGCCAACAATAACACGTACTG  
 GTGCATGAGGACCATCAATGAGACTCACAATTTCTTCTGTGAATTTGCAACTGGCTT  
 CCTAGAGTACTTTGATCTCAACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACT  
 GGACAGGGATGTCCTCAACCAGCTACACGTACAGCTCATGGAGCTGAGGAGCTGCAAGGG  
 TTACAAGCAGTGTAACCCCCGGACTCGAAACATGGACCTGGATGGAGGAAGCTATGAGCA  
 ATACAGGCAGTTTCAGCGTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCCAAATCACT  
 GGGACAACCTGTGGGAAGGCTGGGAAGGTTAAGAAACAACAGAGGTGGACCTCCAAAAACA  
 TAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACC  
 TGTGCTATTGGCCAGGAGGCCTGAGAAAGCAAGCACGCACTCTCAGTCAACATGACAGAT  
 TCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTTTGCCCCCTGCTT  
 TTGCTTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTTCGTATCAAAAAGTCAC  
 CACTAACCCCTCCCCCAGAAGCTCACAAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTTT  
 CTTGGAAATTTCTCCCAAGGGCGAAAGTCATTGGAATTTTTTAAATCATAGGGGAAAAGCA  
 GTCCTGTTCTAAATCCTCTTATTCTTTTGGTTTGTACAAAGAAGGAACCTAAGAAGCAGG  
 ACAGAGGCAACGTGGAGAGGCTGAAAACAGTGCAGAGACGTTTGACAATGAGTCAGTAGC  
 ACAAAGAGATGACATTTACCTAGCACTATAAACCCCTGGTTGCCTCTGAAGAACTGCCT  
 TCATTGTATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTTAGGGGAACCTAA  
 TAAGAAATCCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTA  
 AAAAA

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## FIGURE 74

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGS  
 MQVMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNECNCSSPSWQA  
 QHESRTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVK  
 EKHGSDYSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFP  
 NASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNM  
 LVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIV  
 LNIDLAPTILDIAGLDIPADMKGKSIKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLL  
 HKRDNDKVDAQEENFLPKYQRVKDLQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGP  
 MRLGGSRALSNLVPKYYGQGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV  
 AIEVDGRVYHVGLGDAAQPRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVT  
 HRCYILENDTVQCDLDLYKSLQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEEC  
 DCHKISYHTQHKGRCLKHRGSSLHPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTC  
 SMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNNTYWCMRTINETHNFLFCEFATGFLE  
 YFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYR  
 QFQRRKWPEMKRPSSKSLGQLWEGWEG

**Important features:**

**Signal peptide:**

amino acids 1-17

**Sulfatases signature 1:**

amino acids 86-99

**Homologous region to sulfatase:**

amino acids 87-106, 133-146, 216-229, 291-320, 365-375

**N-glycosylation sites:**

amino acids 65-69, 112-116, 132-136, 149-153, 171-175,  
 198-202, 241-245, 561-565, 608-612, 717-721, 754-758,  
 764-768

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## FIGURE 75

CCCACGCGTCCGCCCACGCGTCCGGTGGACTATGGGCCAGTTTTTTGTGCAAGAACCAGAT  
 GATATTATTTTTTCCAACCTGATTCTGATGAAAAGAAGGTAGCATTGAATTGTGAAGTTTCGT  
 GGCAATCCAGTTCCAGTTACAGATGGCTTCGAAATGGAACAGAAATAGATCTGGAAAGT  
 GATTATCGCTACAGTTTGATAGATGGCACCTTCATTATAAGCAATCCAAGTGAAGCAAAG  
 GATTCTGGTCATTATCAGTGTTTAGCAACCAACACTGTGGGGAGTATTCTTAGTAGAGAA  
 GCTACACTGCAGTTTGCCTATCTGGGAAATTTTAGTGGCCGGACAAGAAGTGCAGTCTCT  
 GTGAGGGAAGGCCAGGGTGTCGTTCTGATGTGCTCTCCTCCGCCACATTCACCAGAGATC  
 ATCTATAGCTGGGTATTTAATGAGTTCCTTTCCTTTGTGGCGGAAGACAGCCGGCGGTTTC  
 ATCTCCCAGGAGACAGGCAACCTTTATATTTCTAAAGTCCAAACATCAGATGTTGGCAGC  
 TATATTTGTCTGGTGAAAAACACAGTGACGAATGCTAGAGTCCTTAGTCCTCCAACGCCA  
 CTCACTCTGCGTAATGATGGTGTGATGGGAGAATATGAGCCGAAAATTGAGGTCCATTTT  
 CCTTTCACGGTTACAGCTGCTAAAGGAACAACCTGTTAAGATGGAATGCTTTGCACTTGGC  
 AACCCCGTTCCAACAATCACATGGATGAAGGTTAATGGTTATATTCCTAGTAAGGCACGT  
 CTGCGGAAATCTCAGGCGGTGCTGGAAATACCGAATGTACAGCTGGATGATGCAGGCATT  
 TATGAGTGCAGAGCTGAAAACCTCACGTGGAAAAAATTCCTTTCGTGGACAATTACAAGTA  
 TACACCTACCCACACTGGGTAGAAAAACTGAATGATACTCAGTTAGACAGTGGGAGCCCT  
 CTCCGATGGGAATGTAAGGCTACTGGAAAACCCAGACCCACGTATCGTTGGCTGAAGAAT  
 GGAGTACCCCTCTCACCTCAGAGTAGGGTTGAGATGGTTAATGGAGTATTGATGATCCAC  
 AATGTGAATCAATCAGATGCTGGAATGTATCAGTGTTTGGCTGAAAATAAGTATGGAGCC  
 ATTTACGCTAGTGCTGAGCTGAAGATTCTAGCTTCAGCTCCCACTTTTGCAGTGAATCAA  
 CTGAAGAAAACAATAATTGTTACCAAAGACCAAGAAGTTGTATAGAGTGCAAACCCCAA  
 GGCTCTCCAAAACCAACCATCTCTTGGAAGAAAGGAGACAGAGCAGTTAGAGAAAAACAA  
 AGAATAGCTATTCTTCCAGACGGGAGTCTACGGATCCTAAATGCTTCCAAATCAGACGAG  
 GGAAAGTACGTTTGCCGAGGGGAAAACGTCTTTGGTTCTGCTGAAAT



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## FIGURE 76

MCSPPPHSPEIIYSWVFNEFPSFVAEDSRRFISQETGNLYISKVQTSADVGSYICLVKNTV  
TNARVLSPPPTPLTLRNDGVMGEYEPKIEVHFPTVTAAGTTVKMECFALGNPVPTITWM  
KVNGYIPSKARLRKSQAVLEIPNVQLDDAGIYECRAENSRGKNSFRGQLQVYTYPHWVEK  
LNDTQLDSGSPLRWECKATGKPRPTYRWLKNVPLSPQSRVEMVNGVLMIHNVNQSDAGM  
YQCLAENKYGAIYASAELKILASAPTFALNQLKKTIIIVTKDQEVVIECKPQGSPKPTISW  
KKGDRVRENKRIAILPDGSLRILNASKSDEGKYVCRGENVFGSAE

**Signal sequence:**

None

**Transmembrane domain:**

None

**N-glycosylation site:**

182-185, 234-237, 325-328

**Tyrosine kinase phosphorylation site:**

328-334

**N-myristoylation site:**

50-55, 150-155, 239-244, 250-255

**Immunoglobulin domain:**

2-56, 100-156, 189-245, 281-338

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## FIGURE 77

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGC  
CGCTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCT  
GGGACAAGAAGCCGCCGCTGCTGCCCGGGCCCGGGAGGGGGCTGGGGCTGGGGCCG  
AGGCGGGGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAA  
TGCTCGGGTGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGC  
CGGCCCGGAGCCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGA  
CCATCCCAACCCGGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGC  
ACCCCATCGCCGGAGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGT  
GGTGGTCCACGTATGGATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGC  
CTTCTCGGACGCGGGGCCCCACGTGCACTACGGCTGGGGCGACCCATCCGCTGCGGCA  
CCTGTACACCTCCGGCCCCACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGG  
CGTCGTGGACTGCGCGCGGGGCCAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGC  
TCTGCGGACCGTGGCCATCAAGGGCGTGCACAGCGTGCGGTACCTCTGCATGGGCGCCGA  
CGGCAAGATGCAGGGGCTGCTTCAGTACTCGGAGGAAGACTGTGCTTTTCGAGGAGGAGAT  
CCGCCCAGATGGCTACAATGTGTACCGATCCGAGAAGCACCGCCTCCCGGTCTCCCTGAG  
CAGTGCCAAACAGCGGCAGCTGTACAAGAACAGAGGCTTTCTTCCACTCTCTCATTTCT  
GCCCATGCTGCCCATGGTCCCAGAGGAGCCTGAGGACCTCAGGGGCCACTTGGAATCTGA  
CATGTTCTCTTCGCCCCCTGGAGACCGACAGCATGGACCCATTTGGGCTTGTCACCGGACT  
GGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACTGAGACCATGCCCGGGCCTCTTAC  
TGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACGTGCTTCTACAAGAACAGTCCTG  
AGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAAGTTGTACATATTAGAGTTT  
TCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGATCATAACATTGTAAGCCTG  
TAGCTTGCCAGCTGCTGCCTGGGCCCCCATCTGCTCCCTCGAGGTTGCTGGACAAGCT  
GCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAACCTCACTTCCTTTGGA  
AAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTCCCCAGGAGCAGC  
CAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTAAAACAGCAGG  
TAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGGACCATTTG  
CCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACCAGGCTTCA  
GGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCCCTGA  
GGCCAGTTCTGTCATGGATGCTGTCTGAGAATAACTTGCTGTGCCGGTGTACCTGCTT  
CCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAG  
ATTTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTA  
GAACCCTTTCCCAGCACTTGCTTTTCCAACATGATATTTATGAGTAATTTATTTTGATA  
TGATACATCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATTTATGTATGTAAGT  
GAGGTTTGTTTTGTATATTAAATGGAGTTTGTGTGT

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## FIGURE 78

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFL  
RIRADGVVDCARGQSAHSLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDC  
AFEEEIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLR  
GHLESDMFSSPLETDSMDPFGLVTGLEAVRSPSF EK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site:**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site:**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 48-59

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## FIGURE 79

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCC  
CTCCCCCGCTTCCCTGTCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCG  
GCCCTGGGGGCTGACAGTCGGCAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTG  
GCGACCAGGCCAGACCAGGGGCGCTCGCTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGT  
GCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAGAGAAGAGTGCGGCGGGACGGAGAAAACA  
ACTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCGCCGCCCTCCCCGGCCCCAGCCC  
TGGGCGCCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCECTTCCGGCA  
CCTCTGGACAGCCAGGATGCTGTTGGCCACCCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCC  
ATCCAGACCGGATTATTTTTTCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGC  
AGGGCACCTTACAGAGGGCCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCA  
TCCTGGGCAGCAAGGAACAGACTGTCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAG  
AGCGCTTAACCCTACGCTCCCCTCTCCAGCCACTGATCTCCCTGTGTGAGGCACCTCCCAGCCCTC  
TGCAGCTGCCCGGGGGCAACGTCACCATCACTTACAGCTATGCTGGGGCCAGAGCACCCATGGGCC  
AGGGCTTCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAGAGTTTCACTGCCTGA  
ACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCTCTGATG  
AAGCAGGTTGAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGCTCCCCTCCTGCCTTGCA  
ATGTCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCT  
CCCACCCCACTGCTGCCATTGGCTGCTGGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCA  
CAGCCCTGGACTTGGGCTTTGGAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCT  
CCCGACTACTGCGTAGTCTCACCCACTTCAGCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTG  
GCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCAATGGTTCGTGGCTTCAATGCCACCTACC  
ATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCTGTGGCTTAGGCTCTGGCCTGGGAGCTGGCG  
AAGGCCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACTGTGCTGACG  
GCACAGATGAGGAGGACTGCCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT  
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTCTGTGTCTGATGGAG  
CAGATGAGAGACGCTGTGCGCATTTGCCAGCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGT  
ATGAGAGCTGGGTGTGCGATGGGCAGCGACTGTGCGGACGGCAGTGATGAGTGAGGACTGCTCCT  
ATGTTCTGCCCCGCAAGGTCATTACAGCTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGG  
TCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCATTGCGACCCAGGAGTACAGCATCTTTGCCC  
CCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCCTTCCCTACGGGCAGCTCATTG  
CCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATAACTCAGTGCTGG  
GCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTGCC  
GCCGTGCTCAGCGGGGCGCTTGATGCGACGCCTGGTACGCCGTCTCCGCCGCTGGGGCTTGCTCC  
CTCGAACCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGTGCTCCCC  
TTGAGGCCCTAGATGGTGCCACAGGTCCAGCCCGTGAGGGCGGGGCGAGTGGGTGGGCAAGATGGGG  
AGCAGGCACCCCACTGCCCATCAAGGCTCCCCTCCCCTCTGCTAGCACGTCTCCAGCCCCACTA  
CTGTCCCTGAAGCCCCAGGGCCACTGCCCTCACTGCCCTTAGAGCCATCACTATTGTCTGGAGTGG  
TGCAGGCCCTGCGAGGCGCCTGTTGCCAGCCTGGGGCCCCCAGGACCAACCCGAGCCCCCTG  
GACCCACACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGGTGCCACTGGCTGAGC  
CGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGGCTCTAC  
TGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCC  
TCCACCACTTCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCCTATGTAG  
CTGCTATAAAGTTAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCA  
TGGCCAGACACCCCACTGCCCTTACCACCCACCTGCTCCCCACGCCACCACCATTTGGGTGGCTGTT  
TTTAAAAAGTAAAGTTCTTAGAGGATCATAGGTCTGGACACTCCATCCTTGCCAAACCTCTACCCA  
AAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGACCCTCCAGCCCCCAAGGGGAGGATTGG  
GGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGGCTCACAAAAAGAGTTGCA  
CAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAGGAATCATA  
CATCTC

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## FIGURE 80

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTQLQRPLVRDSRTSPANCTWL  
 ILGSKEQTVTIRFQKLHLACGSERITLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAG  
 ARAPMGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDEAGCSSDPFP  
 GLTPRPVPSLPCNVTLEDIFYGVFSSPGYTHLASVSHPPQSCHWLLDPHDGRRRLAVRFTALD  
 LGFGDAVHVYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNA  
 TYHVRGYCLPWDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGH  
 FPCGAAGTSGATACYPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDG  
 QPDCADGSDEWDCSYVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPL  
 SRMEAEIVQQQAPPSYGQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGG  
 GPGARRRQRGRMLMRRLLVRRLLRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAR  
 EGGAVGGQDGEQAPPLPIKAPLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRG  
 RLLPSLGPFGPTRSPGPHTA VLAEDEDDVLLVPLAEPGVWVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins:**

amino acids 411-431, 152-171, 331-350 and 374-393

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# FIGURE 81

CTTCTGTGCTGTTTCCTTCTTGCCTCTAACTTGTAACAAGACGTACTAGGACGATGCTAA  
 TGGAAAGTCACAAACCGCTGGGTTTTTGAAGGATCCTTGGGACCTCATGCACATTTGTG  
 GAAACTGGATGGAGAGATTTGGGGAAGC**ATGG**ACTCTTTAGCCAGCTTAGTTCTCTGTGG  
 AGTCAGCTTGCTCCTTTCTGGAAGTGTGGAAGGTGCCATGGACTTGATCTTGATCAATTC  
 CCTACCTCTTGTATCTGATGCTGAAACATCTCTCACCTGCATTGCCTCTGGGTGGCGCCC  
 CCATGAGCCCATCACCATAGGAAGGGACTTTGAAGCCTTAATGAACCAGCACCAGGATCC  
 GCTGGAAGTTACTCAAGATGTGACCAGAGAATGGGCTAAAAAAGTTGTTTGGGAAGAGAGA  
 AAAGGCTAGTAAGATCAATGGTGCTTATTTCTGTGAAGGCGGAGTTTCGAGGAGAGGCAAT  
 CAGGATACGAACCATGAAGATGCGTCAACAAGCTTCCTTCCCTACCAGCTACTTTAACTAT  
 GACTGTGGACAAGGGAGATAACGTGAACATATCTTTCAAAAAGGTATTGATTAAAGAAGA  
 AGATGCAGTGATTTACAAAAATGGTTCCTTCATCCATTCAGTGCCCCGGCATGAAGTACC  
 TGATATTCTAGAAGTACACCTGCCTCATGCTCAGCCCCAGGATGCTGGAGTGTAATCGGC  
 CAGGTATATAGGAGGAAACCTCTTCACCTCGGCCTTCACCAGGCTGATAGTCCGGAGATG  
 TGAAGCCCAGAAGTGGGGACCTGAATGCAACCATCTCTGTACTGCTTGATGAACAATGG  
 TGTCTGCCATGAAGATACTGGAGAATGCATTTGCCCTCCTGGGTTTATGGGAAGGACGTG  
 TGAGAAGGCTTGTGAAGTGCACACGTTTGGCAGAACTTGTAAGAAAGGTGCAGTGAGACA  
 AGAGGGATGCAAGTCTTATGTGTTCTGTCTCCCTGACCCCTATGGGTGTTTCTGTGCCAC  
 AGGCTGGAAGGGTCTGCAGTGCAATGAAGCATGCCACCCTGGTTTTTACGGGCCAGATTG  
 TAAGCTTAGGTGCAGCTGCAACAATGGGGAGATGTGTGATCGCTTCCAAGGATGTCTCTG  
 CTCTCCAGGATGGCAGGGGCTCCAGTGTGAGAGAGAAGGCATACCGAGGATGACCCCAA  
 GATAGTGGATTTGCCAGATCATATAGAAGTAAACAGTGGTAAATTTAATCCCATTTGCAA  
 AGCTTCTGGCTGGCCGCTACCTACTAATGAAGAAATGACCCTGGTGAAGCCGGATGGGAC  
 AGTGCTCCATCCAAAAGACTTTAACCATACGGATCATTTCTCAGTAGCCATATTCACCAT  
 CCACCGGATCCTCCCCCTGACTCAGGAGTTTGGGTCTGCAGTGTGAACACAGTGGCTGG  
 GATGGTGGAAAAGCCCTTCAACATTTCTGTAAAGTTCTTCCAAAGCCCTGAATGCCCC  
 AAACGTGATTGACACTGGACATAACTTTGTGTGTCATCAACATCAGCTCTGAGCCTTACTT  
 TTGGGCAACATATTCAAGTGACAAATGAGATTGTTACACTCAACTATTTGGAACCTCGGAC  
 AGAATATGAATCTGTGTGCAACTGGTCCGTGCTGGAGAGGGTGGGGAAGGGCATCCTGG  
 ACCTGTGAGACGCTTCACAACAGCTTCTATCGGACTCCCTCCTCCAAGAGGTCTAAATCT  
 CCTGCCTAAAAGTCAGACCACTCTAAATTTGACCTGGCAACCAATATTTCCAAGCTCGGA  
 AGATGACTTTTATGTTGAAGTGGAGAGAAGGTCTGTGCAAAAAAGTGATCAGCAGAATAT  
 TAAAGTTCCAGGCAACTTGACTTCGGTGCTACTTAACAACCTTACATCCCAGGGAGCAGTA  
 CGTGGTCCGAGCTAGAGTCAACACCAAGGCCCAGGGGAATGGAGTGAAGATCTCACTGC  
 TTGGACCCTTAGTGACATTCTTCCTCCTCAACCAGAAAACATCAAGATTTCCAACATTAC  
 AACTCCTCGGCTGTGATTTCTTGGACAATATTGGATGGCTATTCTATTTCTTCTATTAC  
 TATCCGTTACAAGGTTCAAGGCAAGAATGAAGACCAGCACGTTGATGTGAAGATAAAGAA  
 TGCCACCATCATTCAGTATCAGCTCAAGGGCCTAGAGCCTGAAACAGCATACCAGGTGGA  
 CATTTTTGTCAGAGAACAACATAGGGTCAAGCAACCCAGCCTTTTCTCATGAACTGGTGAC  
 CCTCCCAGAATCTCAAGCACCAGCGGACCTCGGAGGGGGGAAGATGCTGCTTATAGCCAT  
 CTTTGGCTCTGCTGGAATGACCTGCCTGACTGTGCTGTTGGCCTTTCTGATCATATTGCA  
 ATTGAAGAGGGCAAATGTGCAAAGGAGAATGGCCCAAGCCTTCCAAAACGTGAGGGAAGA  
 ACCAGCTGTGCAGTTCAACTCAGGGACTCTGGCCCTAAACAGGAAGGTCAAAAACAACCC  
 AGATCCTACAATTTATCCAGTGCTTGACTGGAATGACATCAAATTTCAAGATGTGATTGG  
 GGAGGGCAATTTTGGCCAAGTTCTTAAGGCGCGCATCAAGAAGGATGGGTTACGGATGGA  
 TGCTGCCATCAAAGAATGAAAGAATATGCCTCCAAGATGATCACAGGGACTTTGCAGG  
 AGAACTGGAAGTTCTTTGTAACTTGACACCATCCAAACATCATCAATCTCTTAGGAGC

ATGTGAACATCGAGGCTACTTGTACCTGGCCATTGAGTACGCGCCCATGGAAACCTTCT  
GGACTTCCCTTCGCAAGAGCCGTGTGCTGGAGACGGACCCAGCATTTGCCATTGCCAATAG  
CACCGCGTCCACACTGTCCTCCCAGCAGCTCCTTCACTTCGCTGCCGACGTGGCCCGGG  
CATGGACTACTTGAGCCAAAAACAGTTTATCCACAGGGATCTGGCTGCCAGAAACATTTT  
AGTTGGTGAAAACTATGTGGCAAAAATAGCAGATTTTGGATTGTCCCGAGGTCAAGAGGT  
GTACGTGAAAAAGACAATGGGAAGGCTCCCAGTGCGCTGGATGGCCATCGAGTCACTGAA  
TTACAGTGTGTACACAACCAACAGTGATGTATGGTCCATATGGTGTGTTACTATGGGAGAT  
TGTTAGCTTAGGAGGCACACCCTACTGCGGGATGACTTGTGCAGAACTCTACGAGAAGCT  
GCCCCAGGGCTACAGACTGGAGAAGCCCCTGAACGTGTGATGATGAGGTGTATGATCTAAT  
GAGACAATGCTGGCGGGAGAAAGCCTTATGAGAGGCCATCATTGCCCAGATATTGGTGTC  
CTTAAACAGAATGTTAGAGGAGCGAAAGACCTACGTGAATACCACGCTTTATGAGAAGTT  
TACTTATGCAGGAATTGACTGTTCTGCTGAAGAAGCGGCCTAGGACAGAACATCTGTATA  
CCCTCTGTTTTCCCTTTCACTGGCATGGGAGACCCTTGACAACTGCTGAGAAAAACATGCCT  
CTGCCAAAGGATGTGATATATAAGTGTACATATGTGCTGGAATTCTAACAAGTCATAGGT  
TAATATTTAAGACACTGAAAAATCTAAGTGATATAAATCAGATTCTTCTCTCATTTTA  
TCCCTCACCTGTAGCATGCCAGTCCCGTTTCATTTAGTCATGTGACCACTCTGTCTTGTG  
TTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTCA  
TTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGG  
ATTTTCTTTTTCTTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAAAGCC  
TGGGTGACATTTGGGAGACATGTGACATTTATATATTGAATTAATATCCCTACATGTATT  
GCACATTGTAAAAAGTTTTAGTTTTGATGAGTTGTGAGTTTACCTTGTATACTGTAGGCA  
CACTTTGCACTGATATATCATGAGTGAATAAATGTCTTGCCTACTCAAAAAAAAAAAAAA

## FIGURE 82

MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD  
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ  
 QASFLPATLTMTVDKGDVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH  
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC  
 ICPPGFMGRRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE  
 ACHPGFYGPDCKLRCSNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE  
 VNKGKFNPKICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG  
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK  
 LLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS  
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV  
 LLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTSLDILPPQOPENIKISNITHSSAVISWT  
 ILDGYSISSITIRYKVQGNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS  
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR  
 MAQAFQNVREEPAVQFNSGTLALNRKVKNPNPDTIYPVLDWNDIKFQDVI GEGNFGQVLK  
 ARIKKGDLRMDAAIKRMKEYASKDDHRDFAGELEVLCCKLGHPNIINLLGACEHRGYLYL  
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF  
 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD  
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPOGYRLEKPLNCDDEVYDLMRQCWREKPY  
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEAA

### Signal sequence:

1-38

### Transmembrane domain:

750-770

### N-glycosylation site:

140-143, 158-161, 399-402, 438-441, 464-467, 560-563, 596-  
 599, 649-652, 691-694, 930-933, 1011-1014, 1104-1107

### cAMP- and cGMP-dependent protein kinase phosphorylation site:

534-537

### Tyrosine kinase phosphorylation site:

149-156, 808-816, 1094-1102

### N-myristoylation site:

18-23, 98-103, 187-192, 196-201, 270-275, 286-291, 295-300,  
 420-425, 595-600, 984-989, 1036-1041, 1041-1046, 1115-1120

### Prokaryotic membrane lipoprotein lipid attachment site:

882-892



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EGF-like domain cysteine pattern signature:

240-251, 287-298, 329-340

Tyrosine protein kinases specific active-site signature:

960-972

Protein kinase domain:

824-1092

Fibronectin type III domain:

444-529, 543-626, 639-724

EGF-like domain:

220-251, 268-298

laminin EGF Laminin EGF-like (Domains III and V):

219-268

Immunoglobulin domain:

156-193

Zinc finger:

295-313

Receptor tyrosine kinase:

844-868, 869-898, 936-982, 986-1024, 1025-1052, 1052-1088

## FIGURE 83

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCA  
GAAAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCT  
GGCTCACAAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTG  
CAGTCAGTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTTCGGACGGCGG  
TAATTTTCTGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCCG  
ACAGTGGAAACAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGG  
AAAACCCCTTCGATCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAG  
TCGCCATAAAGTATGCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAG  
GCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATT  
ATCCACCTGCAAGCAGTGCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCA  
TACCTACTCTTTTCAGTGCAAACCTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTC  
AGTCAAATGTGAAGGACATTGCCCATGTCTTCAGATAAGCCCACCAGTACAAGCAGAAA  
TGTTAAGAGAGCATGCAGTGACCTGGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTG  
GTTCAAGGCCCTTCATGAAAGTGGAAGTCAAAACAAGAAGACAAAAACATTGCTGAGGCC  
TGAGAGAAGCAGATTCGATACCAGCATCTTGCCAATTTGCAAGGACTCACTTGGCTGGAT  
GTTTAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCAT  
TTACCTTGATAAGAATGAACAGTGTACCAAGGCATTCTTCAATTCTTGTGACACATACAA  
GGACAGTTTAATATCTAATAATGAGTGGTGCTACTGCTTCCAGAGACAGCAAGACCCACC  
TTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCAAGGGGTAAAGAAGCTCCTAGGACA  
GTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT  
TGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTCATGGGATCCAGAATAAATGG  
TGTTGCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCA  
TGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATGATGAAGATGAAATTGA  
AGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTATGACCATGATGTATACAT  
TGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTACAAAAATGATAG  
CCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCACATATATTTT  
GTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTTAAATAAGAATCA  
TTTGCTTTGAGTTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGTCTAGTCAGA  
CAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTCACGAGAACAACTTTGTAAAT  
CTTCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTAAATTTTTTTGAAAGAT  
AATTCTAAGTGAATTTTAAATAAATAAATTTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTC  
AGGATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

amino acids 353-365 and 339-352

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## FIGURE 85

CCCACGCGTCCGGCACTGCAGTCTCCAGCCTGAGCCATGGGCCGCCGAGCCCTCCTGCTC  
 CTGCTTCTGTCTTTTCTGGCGCCCTGGGCCACCATAGCCCTCCGGCCGGCCTTAAGGGCC  
 CTCGGCAGCCTACACTTGCCAACCAACCCACATCCCTCCCGGCTGTAGCCAAGAACTAT  
 TCGGTTCTCTACTTCCAACAGAAGGTTGATCATTTTGGATTTAATACTGTGAAAACTTT  
 AATCAGCGGTACCTAGTAGCTGATAAATACTGGAAGAAAAATGGTGGATCAATACTTTT  
 TACACTGGTAATGAAGGGGACATTATCTGGTTTTGTAATAACACGGGGTTCATGTGGGAT  
 GTGGCTGAGGAAGTGAAGCTATGTTGGTGTGTTGCTGAACATCGATACTATGGAGAGTCT  
 CTCCCCTTTGGTGACAACCTCATTCAAGGATTCAGACACTTGAATTTCTTGACATCAGAA  
 CAAGCTCTGGCTGATTTTGCAGAGTTAATCAAACACTTGAAAAGAACAATCCCAGGAGCT  
 GAAAATCAACCTGTCAATTGCCATAGGAGGCTCCTATGGTGGCATGCTTGCCGCCTGGTTT  
 AGGATGAAATATCCTCATATGGTAGTTGGAGCTCTTGCAGCTTCTGCCCCATCTGGCAG  
 TTTGAGGATTTAGTACCTTGTGGTGTATTTATGAAGATCGTAACCTACAGATTTTAGGAAA  
 AGCGGTCCACATTGTTTCAGAGAGCATCCACAGGTCTTGGGATGCCATTAATCGACTCTCA  
 AATACTGGCAGTGGTTTTGCAGTGGCTTACTGGAGCCCTTCACTTATGCAGCCCATTAACT  
 TCTCAGGACATCCAACATTTGAAAGACTGGATCTCTGAAACCTGGGTGAATCTGGCAATG  
 GTGGACTATCCTTATGCCTCTAACTTTTTACAGCCTTTGCCTGCTTGGCCTATCAAGGTA  
 GTGTGCCAGTATTTGAAAAATCCCAATGTATCTGATTCACTGCTGCTGCAGAATATTTTC  
 CAAGCTCTGAATGTATATTACAATTATTCGGGCCAGGTGAAATGCCTGAATATTTTCAGAG  
 ACAGCAACTAGCAGTCTGGGAACACTGGGTTGGAGCTATCAGGCCTGCACAGAAGTAGTC  
 ATGCCCTTTTGTACTAATGGTGTGATGACATGTTTGAACCTCACTCATGGAACCTTAAAG  
 GAACTTTCTGATGACTGTTTTCAACAGTGGGGTGTGAGACCAAGGCCCTCCTGGATCACT  
 ACTATGTATGGAGGCCAAAACATTAGTTCACACACAAACATTGTTTTTCAGCAATGGTGAA  
 CTAGACCCCTGGTCAGGAGGTGGAGTAACTAAGGATATCACAGACACTCTGGTTGCAGTC  
 ACCATCTCAGAGGGGGCCCACTTAGATCTCCGCACCAAGAATGCCTTGGATCCTATG  
 TCTGTGCTGTTAGCCCGCTCCTTGGAAGTTAGACATATGAAGAATTGGATCAGAGATTT  
 TATGACAGTGCGGGAAAGCAGCACTTGAGAACTTTTGATTGTTTTCAATTTCTTCTTTTA  
 TGTTACACCACCACATTTCCATTCACTTTGATTTTCTACATGTAATTACCTTCTTTTGT  
 TTATCATTAGATTTGATGGGGCCAAAGTTGAGATAGAATAGAGGGTGATGACGGTAAGAG  
 CAAGTGTCCCATGAATGTGATTTCTGGGTTCTCACTGTCCTTTGCACCACGTCTAGGAA  
 GAATCTTCTTGATAGCTCTCCACACCATCAGTGGCCCTCATAACTGGAGTAGAGTTCCT  
 GGTGCTTTTCATAAGAGGGAGAGTTACTTTC

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## FIGURE 86

MGRRALLLLLLSFLAPWATIALRPALRALGSLHLPTNPTSLPAVAKNYSVLYFQQKVDHF  
 GFNTVKTFNQRYLVADKYWKKNNGSILFYTGNEGDI IWFCNNTGFMWDVAEELKAMLVFA  
 EHRYYGESLPFGDNSFKDSRHLNFLTSEQALADFAELIKHLKRTIPGAENQPVIAIGGSY  
 GGMLAAWFRMKYPHVMVGALAASAPIWQFEDLVPCGVFMKIVTTDFRKSGPHCSESIHRS  
 WDAINRLSNTGSGLQWLTGALHLCSPLTSQDIQHLKDWISETWVNLAMVDYPYASNFLQP  
 LPAWPIKVVVCQYLKNPNVSDSLLLQNI FQALNVYYNYSGQVKCLNISETATSSLGTLGWS  
 YQACTEVVMPFCTNGVDDMFEPHSWNLKELSDDCFQQWGVRRPRPSWITTMYGKKNISSHT  
 NIVFSNGELDPWSGGGVTKDITDTLVAVTISEGAHHLDLRTKNALDPMSVLLARSLEVRH  
 MKNWIRDFYDSAGKQH

**Signal sequence:**

1-18

**Transmembrane domain:**

None

**N-glycosylation site:**

47-50, 101-104, 317-320, 336-339, 345-348, 415-418

**Glycosaminoglycan attachment site:**

433-436

**N-myristoylation site:**

178-183, 181-186, 182-187, 198-203, 339-344, 434-439

**Amidation site:**

1-4

**alpha/beta hydrolase fold:**

115-372

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## FIGURE 87

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGT  
GATATTGACAACTGAAGCTTTCTGACCACTGGACTTAAGGAAGAGTGTAATCGTAGG  
CGGACAGCTTTAGTGCGCGGCGCGGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGT  
ACTGACCAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATT  
GAAACTACAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTG  
CAGAAATTTTATCCAACCTTTGTTTGGGAAGCTTATTATGACAATACCATTTTTCATAGAGT  
TGTGCCTGGTTTTCATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTC  
TATCTATGGAGCGCCATTCAAAGATGAATTTTCATTACGGTTGCGTTTTTAATCGGAGAGG  
ACTGGTTGCCATGGCAAATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACT  
GGGTCGAGCAGATGAACTTAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATAC  
AGTATATAACATGTTGCGACTGTCAGAAGTAGACATTGATGATGACGAAAGACCATATAA  
TCCACACAAAATAAAAAGCTGTGAGGTTTTGTTTAATCCTTTTGATGACATCATTTCCAAG  
GGAAATTTAAAGGCTGAAAAAGAGAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAA  
AGGCACAAAAAATTTTAGTTTTACTTTTCATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGA  
AGTAAATCGAGTTAGTCAGAGCATGAAGGGCAAAAGCAAAAGTAGTCATGACTTGCTTAA  
GGATGATCCACATCTCAGTTCTGTTCCAGTTGTAGAAAGTGAAAAAGGTGATGCACCAGA  
TTTAGTTGATGATGGAGAAGATGAAAGTGCAGAGCATGATGAATATATTGATGGTGTATGA  
AAAGAACCTGATGAGAGAAAGAATTGCCAAAAAATTAAGGACACAAGTGCGAATGT  
TAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATCAGTCAGCCGCAGTGAAGAGCTCAG  
AAAAGAAGCAAGACAATTAAACGGGAACCTTAGCAGCAAAACAAAAAAAAGTAGAAAA  
TGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAAGCCCCCTCCAGATGGTGTCTGT  
TGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAGGAAGCAACAGTCAAAGAA  
GGGAACCTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGTTTAAATCTAAACTCAC  
TCAAGCAATTGCTGAAACACCTGAAAATGACATTCTTGAAACAGAAGTAGAAGATGATGA  
AGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGTGAAAGATGCAAG  
CATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGAATAAAAGAAG  
GAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATATAAATGAGAATAA  
TGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTGTTCCCA  
ACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTGAAAA  
ACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGGTA  
CATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAAATTTTCT  
TCCACAAAAA

amino acids 96-140, 49-89 and 22-51

## FIGURE 89

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACG**ATG**CTGCAGGGCCCTGG  
 CTCGCTGCTGCTGCTCTTCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTT  
 CCTCTTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAA  
 CCTGCAGCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCA  
 CGAGACCATGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCA  
 GTGCCACCCGGACACCAAGAAGTTCCTGTGCTCGCTCTTTCGCCCCCGTCTGCCTCGATGA  
 CCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGC  
 CCCGGTCATGTCCGCCTTCGGCTTCCCCTGGCCCCGACATGCTTGAGTGCGACCGTTTCCC  
 CCAGGACAACGACCTTTGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGA  
 GGAAGCTCCAAAGGTATGTGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAAT  
 GGAAACGCTTTGTAAAAATGATTTTGCACCTGAAAATAAAAGTGAAGGAGATAACCTACAT  
 CAACCGAGATACCAAAATCATCCTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGG  
 TGTGTCCGAAAGGGACCTGAAGAAATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCAC  
 CTGTGAGGAGATGAACGACATCAACGCGCCCTATCTGGTCATGGGACAGAAACAGGGTGG  
 GGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAGAAGGGGCAGAGAGAGTTCAAGCGCAT  
 CTCCCGCAGCATCCGCAAGCTGCAGTGCT**AGT**CCCGGCATCCTGATGGCTCCGACAGGCC  
 TGCTCCAGAGCACGGCTGACCATTTCTGCTCCGGGATCTCAGCTCCCGTTCCCCAAGCAC  
 ACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCTTCCCCCTGCCTTTTGCACGTTTGCAT  
 CCCCAGCATTTCTTGAGTTATAAGGCCACAGGAGTGGATAGCTGTTTTTACCTAAAGGAA  
 AAGCCCACCCGAATCTTGTAGAAATATTCAAATAATAAAATCATGAATATTTTAA



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## FIGURE 90

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRL  
PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHS LCVQ  
VKDRCAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKND  
DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSE RDLKKSVLWLK  
DSLQCTCEEMNDINAPYLVMGQKQGELVITSVKRWQKGQREFKRISR SIRQKQC

**Important features:**

**Signal peptide:**  
amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus:**  
amino acids 6-153

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## FIGURE 91

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAG  
GGTCTCGCTCTGTACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTC  
CACCTCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGT  
GGTGACTTCCAAGAGTGACTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACG  
AACTGTTTCTGCTGAGTCTGCTCTTCTGGTCCAAGGTGCCACGGCAGGGGCCACAGG  
GAAGACTTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAA  
CCCACACCAGACCTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCC  
CCTTTCCCTGCAGCCCACCCTGCTTCCCGATCCTTCCCTGACCCCAGGGGCCTCTACCAC  
TTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGAC  
TTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG  
GCTCAGGGCCCCCGCTGTAGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATC  
AGCCTGCCCAGTGCCGCCAGCTTCACTTCTCCTTCCACAGTCCTCCCCACACGGCCGCT  
CACAATGCCTCGGTGGACATGTGCGAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTC  
CTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCCCGCCAGCCAGCAGTTG  
CAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTATGGGGGACATGGTGTCTTCGAG  
GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCACAGCCGGCCTCCAGGACCTG  
CACATCCACTCCCGGCAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTG  
CCTCGAACACTCTTCCAGAGGACGAAAGGCCGGAGCGGGGAGGCTGAGAAGAGACTCCTC  
CTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGACAAGAATTCCAGCCAAGTCCTGGGT  
GAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACCTCACGGAGCCCGTG  
GTGCTCACTTTCCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGG  
GTTGAAGACCCACATTGAGCAGCCCGGGGCATTGGAGCAGTGTGGGTGTGAGACCGTC  
AGGAGAGAAACCCAAACATCCTGCTTCTGCAACCACTTGACCTACTTTGCAGTCTGATG  
GTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGCCTCCTCTCCTACGTG  
GGCTGTGTGCTCTCTGCCCTGGCCTGCCTTGTACCACTTGGCCGCTACCTCTGCTCCAGG  
GTGCCCTGCCGTGCAGGAGGAAACCTCGGACTACACCATCAAGGTGCACATGAACCTG  
CTGCTGGCCGTCTTCTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACA  
GGCTCTGAGGTGGCTGCCGAGCCAGTGCCATCTTCTGCACTTCTCCCTGCTCACCTGC  
CTTCTGAGGTGGCTGCCGAGCCAGTGCCATCTTCTGCACTTCTCCCTGCTCACCTGC  
ACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT  
CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACATATGGCCCCATCATCTTGGCTGTG  
CATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTC  
AGCTACATCACCAACCTGGGCCCTCTTCAGCCTGGTGTCTTCTGTTCAACATGGCCATGCTA  
GCCACCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAAAAGTGGTCACATGTG  
CTGACACTGCTGGGCCTCAGCCTGGTCCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCC  
TTTGCTTCTGGCACCTTCCAGCTTGTGCTCCTCTACCTTTTCAGCATCATCACCTCCTTC  
CAAGGCTTCTCATCTTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCC  
TCCCCTCTGAAGAGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACCTCG  
TCCAGCCGCATCTAGGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTC  
GTCGCACACTGCCTGTGGCCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAGCCGCAGACT  
TTGGAAAGCCCAACGACCATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCGGGC  
TGGGCTTTTGAATTGGCCTTGGGGACTACTCGGCTCTCACTCAGCTCCCACGGGACTCAG  
AAGTGCGCCGCCATGCTGCCTAGGGTACTGTCCCCACATCTGTCCCAACCCAGCTGGAGG  
CCTGGTCTCTCCTTACAACCCCTGGGCCAGCCCTCATTGCTGGGGGCCAGGCCTTGGAT  
CTTGAGGGTCTGGCACATCCTTAATCCTGTGCCCTGCCTGGGACAGAAATGTGGCTCCA  
GTTGCTCTGTCTCTCGTGGTCAACCTGAGGGCACTCTGCATCCTCTGTCAATTTAACCTC  
AGGTGGCACCCAGGGCGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGA



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## FIGURE 92

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIEN  
 SEEALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLL  
 CFQHQEESLAQGPPLLATSVTSWSPQNI SLPSAASF TFSFHSPHTAAHNASVDMCELK  
 RDLQLLSQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKL  
 QPTAGLQDLHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQ  
 DKNSSQVLGEKVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGH  
 WSSAGCETVRRETQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGCVV SALACLV  
 TIAAYLCSRVP LPCRKRPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI  
 FLHFSLLTCLSWMGLEGYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVD  
 NYGPIILAVHRTPEGVIYPSMCWIRDSLVS YITNLGLFSLVFLFN MAMLATMVVQILRLR  
 PHTQKWSHVL TLLGLSLVLGLPWALIFFSFASGT FQLVVLYLFSIITSFQGFLIFIWYWS  
 MRLQARGGPSPLKSNSDSARLPISSGSTSSSRI

### Important features:

#### Signal peptide:

amino acids 1-25

#### Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537,  
 568-590 and 634-657

#### Microbodies C-terminal targeting signal:

amino acids 691-693

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 198-201 and 370-373

#### N-glycosylation sites:

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-  
 327 and 341-344

#### G-protein coupled receptors family 2 proteins:

amino acids 475-504

# FIGURE 93

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCT  
 CTCTTCTCCTTTTGCCCAAACCTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGC  
 CAAGACCAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGT  
 TTTCACCATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTC  
 TTGCTACAGAAAGATACTAAAAGATCACAACTGTACAACTTCCGGAAGGAGTAGCTGA  
 CCTGACACAGATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGAT  
 GATCTGTTACTGCAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACC  
 AAAGATCTCTTTCGTGATTCCTTGCAACAATCAATGGAAATCTTCATGTATTCTGGAGAA  
 CACCATTCTGATTTCCCACAAACCTGCACTACATCAGTATAACTGCATTTCTAGTTTCTA  
 TATAGTGCAATAGAGCATAGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGT  
 GTTAAACAAGTAGTAATAAAAGTTAATTCAATCTAAAAAAAAAAAAA



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## FIGURE 95

GAATTCCGGGCCCCAGGATGCCAACTTTGAATAGGATGAAGACTACAACCTTGTTCCCTTC  
TCATCTGCATCTCCCTGCTCCAGCTGATGGTCCCAGTGAATACTGATGAGACCATAGAGA  
TTATCGTGGAGAATAAGGTCAAGGAACTTCTTGCCAATCCAGCTAACTATCCCTCCACTG  
TAACGAAGACTCTCTCTTGCACTAGTGTCAAGACTATGAACAGATGGGCCTCCTGCCCTG  
CTGGGATGACTGCTACTGGGTGTGCTTGTGGCTTTGCCTGTGGATCTTGGGAGATCCAGA  
GTGGAGATACTTGCAACTGCCTGTGCTTACTCGTTGACTGGACCACTGCCCCTGCTGCC  
AACTGTCCTTAAGAATGAAGAGGTGGAGAACCCAGCTTTGATATGATGAATCTAACAAAAA  
CTGCAGTCTCAATTTGGAAATCTGACTCATGTGCCTTTAAATGTGTTTATATTGCCCATTT  
TACCCTGCTTCTTGAAATGCTTCTTGAAAAATAAAGACAAATTTGCATGTG

MKTTTCSLLICISLLQLMVPVNTDETIEIIVENKVKELLANPANYPSTVTKTLSCTSVK  
TMNRWASCPAGMTATGCACGFACGSWEIQSGDTCNCLCLLVDTTARCCQLS



## FIGURE 97

GAGGCAGAAAGGCAGAAAGGAGAAAATTTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCC  
 CTGCCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAAATGATCCATTCCC  
 TGTGGTCACTTATTCTAAAGGCCCAACCTTCAAAGTTCAAGTAGTGATATGATGACTC  
 CACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACT  
 GAAGGAGTGTGTTTTCCATCCTCCCACGGAAGGAAAGCCCCCTCTGTCCGATCCTCCAAAGA  
 CGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGT  
 GTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCA  
 GGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGA  
 AGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAA  
 CTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCA  
 AGACTGCTTGCAACTGATTGCAGACAGTGAAACACCAACTATACAAAAAGGATCTTACAC  
 ATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAA  
 AATATTGGTCAAAGAACTGGTTACTTTTTTATATATGGTCAGGTTTTATATACTGATAA  
 GACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATT  
 GAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACACTACCCAATAATTC  
 CTGCTATTTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTCCAACCTTGCAATACC  
 AAGAGAAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTTGGTGCATTGAAACT  
 GCTGTGACCCTACTTACACCATGTCTGTAGCTATTTTCTCCCTTTCTCTGTACCTCTAAG  
 AAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAA

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## FIGURE 98

MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC  
LTVVSFYQVAALQGD LASLRAELQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP  
GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL EE  
KENKILVKETGYFFIYGQVLYTDKTYAMGH LIQRKKVHVFGDELSLVTLFRCIQNMPETL  
PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL

**Transmembrane domain:**

amino acids 47-72

**N-glycosylation site:**

amino acids 124-127, 242-245

**cAMP- and cGMP-dependent protein kinase phosphorylation  
site:**

amino acids 33-36, 173-176

**N-myristoylation site:**

amino acids 96-101

**TNF family proteins:**

amino acids 172-206

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## FIGURE 100

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAQAQRCFCQVSGYLDDCTCDVETIDRFNNYR  
 LFPRLQKLLESDYFRYYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVDPDGIKSASYKY  
 SEEANNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVD  
 LLLNPERYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGL  
 CVEKRAFYRLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRR  
 LKNLYFLYLIELRALSKVLPPFFERPDLFTGNKIQDEENKMLLLEILHEIKSFPLHFDE  
 NSFFAGDKKEAHKLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKL  
 IANMPESGPSYEFHLTRQEIIVSLFNAFGRISTSVKELENFRNLLQNIH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site:**

amino acids 280-283 and 384-387

**Amidation site:**

amino acids 94-97

**Glycosaminoglycan attachment site:**

amino acids 20-23 and 223-226

**Aminotransferases class-V pyridoxal-phosphate:**

amino acids 216-222

**Interleukin-7 proteins:**

amino acids 338-343

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**FIGURE 101**

GCCTAGCCAGGCCAAGAATGCAATTGCCCCGGTGGTGGGAGCTGGGAGACCCCTGTGCTT  
GGACGGGACAGGGTCGGGGGACACGCAGGATGAGCCCCGCGACCACTGGCACATTCTTGC  
TGACAGTGTACAGTATTTTCTCCAAGGTACACTCCGATCGGAATGTATACCCATCAGCAG  
GTGTCCTCTTTGTTTCATGTTTTGGAAAGAGAATATTTTAAGGGGGAATTTCCACCTTACC  
CAAAACCTGGCGAGATTAGTAATGATCCATAACATTTAATACAAATTTAATGGGTACC  
CAGACCGACCTGGATGGCTTCGATATATCCAAAGGACACCATATAGTGATGGAGTCCTAT  
ATGGGTCCCCAACAGCTGAAAATGTGGGGAAGCCAACAATCATTGAGATAACTGCCTACA  
ACAGGCGCACCTTTGAGACTGCAAGGCATAATTTGATAATTAATATAATGTCTGCAGAAG  
ACTTCCCGTTGCCATATCAAGCAGAATTCCTTCATTAAGAATATGAATGTAGAAGAAATGT  
TGGCCAGTGAGGTTCTTGGGAGACTTTCTTGGCGCAGTGAAAAATGTGTGGCAGCCAGAGC  
GCCTGAACGCCATAAACATCACATCGGCCCTAGACAGGGGTGGCAGGGTGGCACTTCCCA  
TTAATGACCTGAAGGAGGGCGTTTATGTCATGGTTGGTGCAGATGTCCCGTTTTCTTCTT  
GTTTACGAGAAGTTGAAAATCCACAGAATCAATTGAGATGTAGTCAAGAAATGGAGCCTG  
TAATAACATGTGATAAAAAATTTCTGACTCAATTTTACATTGACTGGTGCAAAATTTTCAT  
TGGTTGATAAAACAAAGCAAGTGTCCACCTATCAGGAAGTGATTCGTGGAGAGGGGATTT  
TACCTGATGGTGGAGAATACAAACCCCTTCTGATTCTTTGAAAAGCAGAGACTATTACA  
CGGATTTCTTAATTACACTGGCTGTGCCCTCGGCAGTGGCACTGGTCCTTTTTCTAATAC  
TTGCTTATATCATGTGCTGCCGACGGGAAGGCGTGGAAAAGAGAAACATGCAACACCAG  
ACATCCAACCTGGTCCATCACAGTGCTATTCAGAAATCTACCAAGGAGCTTCGAGACATGT  
CCAAGAATAGAGAGATAGCATGGCCCCCTGTCAACGCTTCCTGTGTTCCACCCTGTGACTG  
GGGAAATCATACTCCTTTACACACAGACAACTATGATAGCACAAACATGCCATTGATGC  
AAACGCAGCAGAACTTGCCACATCAGACTCAGATTCCCCAACAGCAGACTACAGGTAAAT  
GGTATCCCTGAAGAAAGAAAACCTGACTGAAGCAATGAATTTATAATCAGACAATATAGCA  
GTTACATCACATTTCTTTTCTCTTCCAATAATGCATGAGCTTTTCTGGCATATGTTATGC  
ATGTTGGCAGTATTAAGTGTATACCAAATAATACAACATAACTTTCATTTTACTAATGTA  
TTTTTTTGTACTTAAAGCATTTTTGACAATTTGTAAAACATTGATGACTTTATATTTGTT  
ACAATAAAAGTTGATCTTTAAAATAAATATTATTAATGAAGCCTAAAAA



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## FIGURE 103

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGT  
 GTGAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTG  
 TGAGGAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCA  
 CCTTTTGCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATA  
 AGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAAAC  
 TAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCC  
 AGGATCTGGGTGCTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATA  
 CTTATGGTGAAGAAGGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCAC  
 ACTTCTTTGGGGATTTTGGTTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATA  
 TTCCAAGAGGAAGTGATATTATTGTAGATCTAGAAGTCACTTTGAAGAAGTATATGCAG  
 GAAATTTTGTGGAAGTAGTTAGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGA  
 AGTGCAATTGTGCGCAAGAGATGCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGA  
 CCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGC  
 TGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGGAGTACCCCTTTATTGGAGAAG  
 GTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCCGAATCAAAGTTGTCAAGC  
 ACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGACAATCTCATTAGTTG  
 AGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACAAGGTACATATTT  
 CCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAGGGCTCCCCA  
 ACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATTTTCCAA  
 AAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGTCAG  
 TGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGT  
 AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTTGTGTGTGTTTTTGT  
 TTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAAT  
 AAGAGGGCTTAAGAATTTGTCCATTTGCATTCGGAAAAGAATGACCAGCAAAAGGTTTAC  
 TAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGTTTCAAGAATTAA  
 AGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCA  
 ATTTCAATTCAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGTTATTTT

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## FIGURE 104

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDD  
PQAQEKFDLGAAYEVLSDSEKQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGT  
PRQQRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQL  
GPGRFQMTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFGEGEHVDGEPGDLR  
FRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLW  
KKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence:**

amino acids 254-257

**Nt-dnaJ domain signature:**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins:**

amino acids 26-58

**N-glycosylation site:**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site:**

amino acids 253-260

**N-myristoylation site:**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site:**

amino acids 164-168



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## FIGURE 105

GGCACGAGGCGGCGGGGCGAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAG  
 GTCTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACT  
 TCCAGCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAA  
 GCATGGAGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTCTGGCTTCGT  
 TTGCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGC  
 GCTATGATTCTAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCT  
 CTGAGTTAGAACTGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGA  
 ATGAAGACTGGATCGAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGA  
 TTTGTCACACTCTGACAGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGA  
 AGACTTCAGCCAGTGTGAGCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGG  
 ATGATGTTGTGAAGTCGATGTACCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGA  
 CTGCCCTGCTCCTGTCTGTGAGTCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGA  
 CGGGAGGCTGGACTGGATTGACCAGTCTCTGTGCGGCTGCTGAGGAGCATTTGGAAGTCC  
 TTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCC  
 TGCAGGAGCAGTCTGCAATTTAGTGCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTGC  
 CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTTCTATAGAGTTAGTTGTTCTC  
 CACGGCTGGAGAGTTTACAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCCGTCAGTTTATG  
 CCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGTGGCAGTCTAATACTACAGTTAGGGGA  
 GATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAACCTGGTGGACTGTCAGCTTTATTTA  
 GCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCTAAGAAATCAAGAGGTTTCACAT  
 TAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATGTGTGGCAATTCTGATCTGCA  
 TTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTCTTCTTTTGGCAAGACTTG  
 TACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCTGGTCCCTGAGGCGTCT  
 GGGTCTCTCCTCTCCCTTGCAGGTTTGGGTTTGAAGCTGAGGAACTACAAAGTTGATGAT  
 TTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCCTAGGTGGATAGTAAATTT  
 ATACTTATGTTTCCCTCAAAAAAAAAAAAAAAAAA



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## FIGURE 107

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGT  
 CCCCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAAAC  
 AGGATTTGGAGTGTTTTTCTGTTCCTTGGGAATGATTCTCTTTTTTGACAAAGCACTACT  
 GGCTATTGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAAC  
 ATTCAGATTCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGT  
 ATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTT  
 TCTCTTGTTCAAGGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCT  
 TGGATCCCTCCTAAATTTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAA  
 CAATATGGTAT**TAA**CAACAAGTGAATTTGAAGACTCATTTAAAATATTGTGTTATTTATAA  
 AGTCATTTGAAGAATATTCAGCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTT  
 TACAGGAGTTTAAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGT  
 GAAAACAGGCTTCTACTCAAGTGAACCTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTTG  
 AAATCCATGTTAATGATGCTTAAGAACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAA  
 TGTGCGAACTCAGCCATCCTTAGAGAACTGTGGTGCCTGTTTCTTTTCTTTTTATTTTG  
 AAGGCTCAGGAGCATCCATAGGCATTTGCTTTTTTAGAAGTGTCCACTGCAATGGCAAAAA  
 TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTTCGATTGGATTGTGTCATT  
 TTAAAGTATTAAAACCAAGGAAACCCCAATTTTGATGTATGGATTACTTTTTTTTNGNCN  
 CAGGGCC

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## FIGURE 108

MISLTDQTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFF  
QKHKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLLN  
LPGIRSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites:**

amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein:**

amino acids 49-59

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## FIGURE 109

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGA  
GCACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGC  
TGGCTGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAG  
GAGTGTCGGACTGTGTCAACATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCA  
CACTCTACTCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCT  
GTGCCAGCAAGTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCT  
GCTGCAATACTGAGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCG  
GGGCCCTCACGCTCCTCCCCTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCAT  
GGCCCTATGCGGCCAGCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAA  
AAAAAAAAA



# FIGURE 111

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCG  
GGCGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCG  
CTCGGCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGC  
CTGGATCGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCA  
GAGCCGGGTCCAGCCCATGACCGCCTCCAAGTGGACGCTGGTGTATGGAGGGCGAGTGGAT  
GCTGAAATTTTACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAATGGGAGGC  
TTTTGCAAAGAATGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGA  
ACCAGGTTTGAGTGGCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGA  
TGGGATATTCCGCCGTTATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTT  
AGAGAAGAAATGGCAATCAGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAAC  
GATGTCCTGGAATGGCTGGTCTTTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAATA  
TTTCACAGTGACTCTTGGAATTCCTGCTTGGTGTCTTATGTGTTTTTTCGTCATAGCCAC  
CTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGT  
GCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCA  
TAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGATTCAAATGAAGAAGAAAA  
CAAAGACAGCCTTGTTAGATGATGAAGAAGAGAAAGAAGATCTTGGCGATGAGGATGAAGC  
AGAGGAAGAAGAGGAGGAGGAGCAACTTGGCTGCTGGTGTGGATGAGGAGAGAAGTGAGGC  
CAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGAGCCTGAGGA  
GGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGCTGACACAGAGGTGGTGGAAAGACTC  
CTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTGTAGATTTAATGATGCGTTTTT  
CAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGGCCTGCAGTTTGTACCAAATC  
CTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCTCTCTAGTCATTTGGTCTC  
ATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAG  
AAAAACAAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAACAAGTTCATTTACT  
TAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATCAGCACCTTCCAG  
AGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATC  
CCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTCTGTGTAAAGTATTTATTTTTGTCA  
AATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAAATTGAA  
AGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTGTGCT  
ATGTTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCTCC  
ACACTCTTCACTATTATCTCTTGGTCAAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTTGTTTATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCT  
GTGACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAG  
GATTTTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAAATATAGTTGTTGTTGATTT  
TTTTTTAAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTAC  
AAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTCATCTCAAGGGGTTCCCTG  
GGTCTTGAAGTACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTTCAGTGATGTG  
CTTTTGGTGAAGAATTAAATGAAGTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTC  
CATCTTCTGTAATCTTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACT  
GTAAGTACCCAGGAGGCTAATTTCTTT

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## FIGURE 112

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFY  
APWGPSCQQTDSWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI  
RFRGPGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVT  
LGIPAWCSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQ  
LQDAEEEEKDDSNNEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQG  
PPGEDGVTRREEVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site:**

amino acids 46-49

**Thioredoxin family proteins:** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins:**

amino acids 173-187



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## FIGURE 113

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAA  
TCCCGTGCGCCGCGGCTGGGCCGTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGC  
TTGGGCTCGGCCAGGCGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGA  
AGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGAAGTATTAGAAATGAG  
CTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT  
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTG  
AATCTTAATGTTCACTTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAA  
TAAAGATGACTATATCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATAT  
GGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGGAGTGTCCAAAACCTGC  
AAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA  
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGT  
ACTCAAAGATGAAGATCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGA  
TAATCAAGGTGGCCAGTATGAAAGCTGGAAGCTTATCGTTATGATTTTGGTATTTATGA  
TGATGATCCTGAAATCATAACATTGGAAGAAGAGAATTTGATGCTGCTGTTAATTCTGG  
AGAATGTGGTTTTGTAAATTTTTACTCCCAGGCTGTTACACTGCCATGATTTAGCTCC  
CACATGGAGAGACTTTTGCTAAAGAAGTGGATGGGTACTTTCGAATTGGAGCTGTAACTG  
TGGTGATGATAGAATGCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCAT  
TTTTCGGTCTGGAATGGCCCCAGTGAAATATCATGGAGACAGATCAAAGGAGAGTTTAGT  
GAGTTTTTGAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTGGACAGGAAATTTTGT  
CAACTCCATACAACTGCTTTTGCTGCTGGTATTGGCTGGCTGATCACTTTTTGTTCAAA  
AGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAA  
CTCATTGGATGCTAAAGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAC  
ACTTTCGGCAAACACACTAGAGGATCGTTTGGCTCATCATCGGTGGCTGTTATTTTTTCA  
TTTTGGAATAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACTAAAACTCTACTTAA  
AAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCTCTGCACCAGACATCTGTAGTAA  
TCTGTATGTTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGA  
AATTCATCATGGAAAGAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAA  
TTCTCATGTTACCACGCTTGGACCTCAAATTTTCTGCCAATGACAAAGAACCATGGCT  
TGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACTACCAGAGTTACGAAG  
AGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCATGA  
GGGACTCTGTAACATGTATAACATTAGGCTTATCCAACAACAGTGGTATTCAACCAGTC  
CAACATTCATGAGTATGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGA  
TCTTATGAATCCTTCAGTGGTCTCCCTTACACCCACCACCTTCAACGAACTAGTTACACA  
AAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTGGTGTATCCTTGCCA  
AGTCTTAATGCCAGAATGGAAGAAGTGGCCCGGACATTAAGTGGAGTATCAACGTGGG  
CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATACCC  
TGAGATAAGATTTTTTCCCCCAAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGG  
TTGGAATAGGGATGCTTATTCCCTGAGAATCTGGGGTCTAGGATTTTTTACCTCAAGTATC  
CACAGATCTAACACCTCAGACTTTCAGTGAAAAAGTTCTACAAGGGAAAAATCATTGGGT  
GATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT  
CTTGGCTAGGATGATTAAAGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGC  
TCAGACATGCCAGAAAGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTTATTCTACGA  
AAGAGCAAAGAGAAATTTTCAAGAAGAGCAGATAAATACCAGAGATGCAAAGCAATCGC  
TGCCTTAATAAGTGAAAAATTGGAAGCTCTCCGAAATCAAGGCAAGAGGAATAAGGATGA  
ACTTTGATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG  
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTT

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GCAGTTGTACTGCCAGAATTATCTACAGCACTGGTGTAAAGAAGGGTCTGCAAACCTTTT  
TCTGTAAAGGGCCGGTTTATAAATATTTTAGACTTTGCAGGCTATAATATATGGTTCACA  
CATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCTTTTAACAACCTTTAA  
AAAATATTAAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTTCAGTCCATG  
GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACA  
TGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCAC  
GTTTTTTGGCTGACCTGAAAAGAGGTAACTTAGTTTTTGGTCACTTGTTCTCCTAAAAAT  
GCTATCCCTAACCATATATTTATATTTTCGTTTTTAAAAACACCCATGATGTGGCACAGTAA  
ACAAACCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCCCTTCTCA  
AAGGTTGAAAAAATGCTTTTAATTTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGC  
ACACAGTAAGTACACAAATTTGAGCAACAGTAAGTGCACAAATTCTGTAGTTTGCTGTAT  
CATCCAGGAAAACCTGAGGGAAAAAATTATAGCAATTAAGTGGGCATTGTAGAGTATCC  
TAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATATGTGTTTCATGTATTT  
TCTGAAATTGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT  
TTACATATTTGCCTTCTGAACTTTGTTTTGACCTGTATCCTTTATTTAATTGGGTTTTT  
CTTTCATAGTTTTGGTTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAAT  
TACTTTACAGGTTGTTTTACTGTAGCTTATAATGATACTGTAGTTATTCCAGTTACTAGT  
TTACTGTCAGAGGGCTGCCTTTTTTTCAGATAAATATTGACATAATAACTGAAGTTATTTTT  
ATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGA  
CTCAAAGAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTAC  
AGAATGGTAAAAATTCCAATCAGTCAAAGAGGTCAATGAATTAAAGGCTTGCAACTTT  
TTCAAAAAAAAAAAAAAAAAA

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## FIGURE 114

MGVWLNKDDYIRD LKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLAL  
 KLHPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYRY  
 DFGIYDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLR  
 IGAVNCGDDRM LCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTEL  
 WTGNFVNSIQTAFAAGIGWLITFC SKGGDCLTSQTRLRLSGMLFNLSDAKEIYLEVIHN  
 LPDFELLSANTLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSA  
 PDICSNLYVFQPSLAVFKGQGTKEYEIHGKILYDILAFAKESVNSHVTTLGPQNFPAN  
 DKEPWLVDFFAPWCPPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTT  
 VVFNQSNIEHEYEGHSAEQILEFIEDLMNP SVVSLTPTTFNELVTQRKHNEVWMVDFYSP  
 WCHPCQVLMPEWKRMARTLTGLINVGSIDCQYHSFCAQENVQRYPEIRFFPPKSNKAYQ  
 YHSYNGWNRDAYSRLIWGLGFLPQVSTD LTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNF  
 APEFELLARMIKGKVKAGKVDCQAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTR  
 DAKAIAALISEKLETLRNQGKRNKDEL

**Important features:**

**Endoplasmic reticulum targeting sequence:**

amino acids 744-747

**Cytochrome c family heme-binding site signature:**

amino acids 158-163

**Nt-dnaJ domain signature:**

amino acids 77-96

**N-glycosylation site:**

amino acids 484-487

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## FIGURE 115

GCGGGCTGTTGACGGCGCTGCG**ATGG**CTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGG  
TTCCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGGGCCCCTTGGGCCGTGCCCAC  
CACTGTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGAC  
GCTGAGCTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAG  
GAAATGGAAGCAACTGTGCGAGATTGCAGCGGAATATGATTCTCTTCCTCCTTGCCCTTTCT  
GCTTTTCTGTGGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTT  
CAGGCTAGAGGAAGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAAACAGCAAATCC  
ACCCGTCTTACCAGCTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCT  
GTCACAGAAGACACAAAGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCC  
AAGCCAAGACCTGAAGGATGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCCTGT  
GGATCCCCGCCCGGAAGGAGATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGAT  
CGAGCCTGAGCAGGGCACCGAGCTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCC  
CCTGCCACCGGCCAGGACACAGGGCACACCAGTGCATCTGAACCTATCGCCAGAAGGGCGT  
GATTGACGTCTTCCTGCATGCATGGAAAGGATAACCGCAAGTTTGCATGGGGCCATGACGA  
GCTGAAGCCTGTGTCCAGGTCCTTCAGTGAGTGGTTTGGCCTCGGTCTCACACTGATCGA  
CGCGCTGGACACCATGTGGATCTTGGGTCTGAGGAAAGAATTTGAGGAAGCCAGGAAGTG  
GGTGTCTGAAGAAGTTACACTTTGAAAAGGACGTGGACGTCAACCTGTTTGAGAGCACGAT  
CCGCATCCTGGGGGGGCTCCTGAGTGCCTACCACCTGTCTGGGGACAGCCTCTTCCTGAG  
GAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGCCTTCAGAACACCATCCAAGATTCC  
TTACTCGGATGTGAACATCGGTACTGGAGTTGCCCACCGCCACGGTGGACCTCCGACAG  
CACTGTGGCCGAGGTGACCAGCATTGAGCTGGAGTTCCGGGAGCTCTCCCGTCTCACAGG  
GGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCACATCCACGGCCTGTCTGG  
GAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTGGCCTCTTCACCCACCT  
GGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTACCTGCTGAAGCAGTG  
GATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGAAGCCATCGAGGG  
TGTCAGAACGCACCTGCTGCGGCACCTCCGAGCCAGTAAGCTCACCTTTGTGGGGGAGCT  
TGCCACGCGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCCTGCCAGGGACGCT  
GGCTCTGGGCGCTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCCAGGAGCTCAT  
GGAGACTTGTTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCGTGCA  
CTTCAACCTTTACCCCCAGCCGGGCCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGGCA  
CAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCCACAGGGGA  
CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACAGGGT  
CCCCCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCGAGCCTAG  
GGACAAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTC  
CGATGACCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCTCT  
GCCTATCTGGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAG  
AGGCACCTTGCTGGGTCTGTGGCATTTCCTCAAGGGCCACGTAGCACCGGCAACCGCCAA  
GTGGCCCAGGCTCTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACC  
GTGAGGACAAGTGAGGCCGTGAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGC  
CTCCGCCGTGCTTCTCCAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAG  
GTCTCTGTGGGCCGACCAGAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAG  
TGGACAGCCCAGGGTGCAGCTCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAA  
GGGTCTGGAGGGGCTGCCGTGACTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGT  
TACAAGCTGGACTCAGGGATCCTCCTGGCCGCCCCGAGGGGGCTTGAGGGCTGGACGG  
CAAGTCCGTCTAGCTCACGGGCCCCCTCCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAG  
TTGATTTGCTCTAACCGCAA

amino acids 21-40 and 84-105 (type II)

GTGGGATTATTATTGTAGTGCAAGATCGTTTTCTCAGTGGTGGTGGGAAGTTGCCTCATCGCA  
GGCAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTT  
AAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCA  
TCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTTGCACCATAACTTCCTCAGCTTGA  
GCAGTTTGTAAAGGAATGAGGTTACAGATTACAGGAATTGTAGGGCCTCAACCTATAGACT  
TTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCA  
TCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACA  
ACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCC  
GGTCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACC  
CTAAACTTTTGGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTT  
TAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACA  
TGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGC  
CAGGACATGCAGCTGCATTTTTCAGAAGATTGTGATTTCAGCCTCTACTAAAGTTGTCATCC  
GTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAATTCT  
GTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGTGCAACCC  
TGACGGAATGGAAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATG  
TAGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTA  
TCGTATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTT  
CCAGTGCTGGAAAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGA  
ATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT  
ATATTCCAGACCCAAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACA  
TAAAGTGAACAGAAATTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTCTGGAAGTACGATAGC  
ATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAA  
GATGTGTACAGTAAAGTAAAGATGACAAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAG  
ACTATAGACTATAAGATATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTG  
AATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGATAAATTCAAAA  
CTGCTGTTGGTTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAAACTTACATTTTTTC



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## FIGURE 119

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAG  
ATCTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCTCTG  
GATGCTGCTTTCCTGCCTCATTCTCCTGTGTCTCAGGTTCAAGGTGAAGAAACCCAGAAGGA  
ACTGCCCTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTA  
TGCCTTGTTTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCC  
CTCTGGAAAACCTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCTCCCTGGT  
GAGGAGCATTAGTAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCCACACAGGG  
CTCTGAGCCTGATGGAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGC  
ATGGGAGAAAAATCCCTCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAG  
CACAGGATTTCTGAAGTGGAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAA  
GTTCAAGGACTTAGGGCAGGTGGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATG  
GACATGAGACCAGTGTGAAGACTCACCTGGAAGAGAATATTCTCCCCAACTGCCCTAC  
CTGACTACCTTGTCATGATCCTCCTTCTTTTTCTTTTTCTTCACCTTCATTTTCAGGCTT  
TTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATAATAAAAATGTTACTTTATAAA  
AAAAAAAAAAAAAAAAAAAA



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FIGURE 120

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKS  
WMDADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGW  
EWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature:

amino acids 146-171

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## FIGURE 121

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTT  
TGGGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAG  
AACAATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAG  
ATGGCTGAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGA  
GTCTACCAAATGAGACCTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTTCATG  
TGGTTTTTCTACGCATTGATTCCATGTTTGTCTACAGATGAAGTGGCCATTCTGCCTGCC  
CCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTG  
ATCGCGCCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCTG  
TACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGT  
GATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTG  
GGCTCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATC  
CTTACCCGACCTGGGATGGAGATCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAG  
GACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAG  
GAACATGTCAAAATGGTGAGGAGTGGGGGTATTCCAGTGCACCTAGAAACCATGGAGCCA  
GGGGCTGCATACTGTGTGAAGGCCCAGACATTTCGTGAAGGCCATTGGGAGGTACAGCGCC  
TTCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCCCCTGGTACTGGCCCTG  
TTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTTCGTGCCACTGTTTCGTCTGGAAAATG  
GGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTTCCTCCCAGACACCTTGAAAATA  
ACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGTGCCACG  
GCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGATCTCATAGGTTTGCAGGAGGGCC  
CAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT  
TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTC  
TAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACTGACTGAGGCTTAGGG  
GATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACCCTGGGAAAAGTGAC  
TTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACCTACACACCTGCT  
AAACACACACACACAGAGTCTCTCTATATATACACACGTACACATAAATACACCCAGC  
ACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTCAAGTGTCTCTG  
GAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGTGGCTTG  
GAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGGTGT  
GAGTTCACCTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGTAG  
GTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACCTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTAT  
GTGTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTT  
TTTCTGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGT  
AAAAAAAAAAAAAAAAA

amino acids 232-262

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## FIGURE 124

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLKYRGSVSLVNVVASECGFT  
DQHYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAV  
TGTGAHPAFKYLAQTSKGPEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLI  
LLKREDL

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## FIGURE 127

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAG  
 CCCTTTCCTAACCCAACCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTAC  
 GGACCCAGCGTTACCAATGCATCCTGCCGTCTTCTTATCCTTACCCGACCTCAGATGCTC  
 CCTTCTGCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGC  
 TACAGAGAATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGC  
 TGA CTGGTGTCTGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCAT  
 TAAGGAAGAATTTCCAAATGAAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCA  
 CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAA  
 TGGGATGATGATGAAGAGAGAATAACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA  
 CATCAGGCAACAAAAAAGTGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCAC  
 TCTTGATCGCAGCAAAAGAAATATCATTGGATATTTTGAGCAAAAGGACTCGGACAAC TA  
 TAGAGTTTTTGAACGAGTAGCGAATATTTTGCATGATGACTGTGCCTTCTTCTGCTATT  
 TGGGGATGTTTCAAACCCGAAAGATATAGTGGCGACAACATAATCTACAAACCACCAGG  
 GCATTCTGCTCCGATATGGTGTACTTGGGAGCTATGACAAATTTTGATGTGACTTACAA  
 TTGGATTCAAGATAAATGTGTTCCTCTTGTCCGAGAAATAACATTTGAAAATGGAGAGGA  
 ATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAAAGAAGATACAGAAAG  
 TTTAGAAATATTCCAGAATGAAGTAGCTCGGCAATTAATAAGTGAAAAAGGTACAATAAA  
 CTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACAGAAAACCTCC  
 AGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGGGAGACTT  
 CAAAGATGTATTAATTCTTGGAAGAACTCAAGCAATTCGTATTTGACTTACATTCTGGAAA  
 ACTGCACAGAGAATTCCATCATGGACCTGACCCAACCTGATACAGCCCCAGGAGAGCAAGC  
 CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATA  
 TAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTGAAAAACAGTTTGTAAG  
 CCTTTC AACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTATATTTTCATAATTC  
 TATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAA



**Thioredoxin family proteins:**  
amino acids 50-66

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## FIGURE 129

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACT  
GCAGGCTGGCTGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGC  
TGCGTGACAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCG  
CCGGGCGTGAGCGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTC  
TCGCTGGCAGTGCGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGAT  
CTTACGGGCTTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCC  
AAGCTCAACCTCACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGACATACCCGCC  
AACGGCGTGAGTGCTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCG  
CCGCCGGTTCGTGAGCTGCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGC  
AACGTCACCTTGACGGCAGCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAG  
GATGAATTCTGCACTCGGGATGGAGTAACAGGCCCAGGGTTACGCTCAGTGGCTCCTGT  
TGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATC  
CCACCCCTTGTCCGGCTGCCCCCTCCAGAGCCACGACTGTGGCCTCAACCACATCTGTC  
ACCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACCACCAAACCCATGCCAGCGCCA  
ACCAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCCCGGGATGAGGAGCCCAGG  
TTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGGCAGTATCCTGCAAAA  
GGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCACAGCTGGATTGGCAGCC  
CTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTGAGCTTCTCCACCTGGAAATTTCCCT  
CTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCTGTTCACCACTG  
GACTGGGCTGGCCAGCCCCTGTTTTTCCAACATTCCCCAGTATCCCAGCTTCTGCTGC  
GCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA  
GCTTTTGGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCTCTTG  
ATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTGAGAGAGAGGATGCTAA  
GCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAA  
TGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCC  
CATATGTCTTCCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTACCCAATTGCGC  
CTATAGTGAGTCGTA



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FIGURE 131

AAACTTGACGCC**ATGA**AAGATCCCGGTCTTCTCTGCCGTGGTGCTCCTCTCCCTCCTGGTG  
CTCCACTCTGCCCAGGGAGCCACCCTGGGTGGTCTTGAGGAAGAAAGCACCATTGAGAAT  
TATGCGTCACGACCCGAGGCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCT  
GCGTTTAAGGCTGATGAGTTCTTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAGGAAA  
CTTCCTTTCTCAACTGGGATGCCTTTCTTAAGCTGAAAGGACTGAGGAGCGCAACTCCT  
GATGCCCAGT**GAC**CATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAA  
CCTACCATAACTCTTTCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

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**FIGURE 132**

MKIPVLPVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFKA  
DEFLNWHALFESIKRKLPFLNWDAFPKLGKGLRSATPDAQ

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**AT**GGGGGTGGAGATT  
GCCTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTT  
GTTCTTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCC  
TGTGGCTTTGCCGGCCACTCA**TGA**GAGTGTTTTTTGTGTAAAGTATTTTTTTAGAATACTGT  
TGACTTCTTCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATG  
TCAACCCTCAAATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTTAAGGT  
CCCTTTATTTTTAGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCAT  
TGATTTTGTTTATCTTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGAC  
CTCTAGGAGAATAATTTTATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCACAAA  
TGTGATTGTTAATTTAAATGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGA  
ATAACCAGAATCTATTTCTTAAAGTTTTGAGTATATTTTTTCAACTAGATATTTGTATAG  
AAAGACTGAATAGTGATG

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## FIGURE 134

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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# FIGURE 135

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGGCTC  
TGGCTGCTGTTGTTTCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAA  
TGGAAAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGT  
CAAACTGCAGCTGCTACCATGGTGTATAGAAAGAGGATCTAACTCCTTTCCGAGGAGGC  
ATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATC  
ACTAAGAACAGACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTT  
GAGCACTTTATTTTGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTA  
CGAGATTATCCTCAGGTTCCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGT  
AAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCT  
GCTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTG  
GTAAGGTCAGCAGCACAGTGGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGA  
TCAAGGACAAGTCCAGAACGAGATCCTCTCATTTCTTGTCTCGGAAAAACCCAAAACCT  
GTTGATGCAGAATACACCAAAAACCAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAG  
CCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAGTATCTGTTTAATTTT  
CGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCCTGTGTGGCTCACTTGTTTTT  
CATGTTGGTGATGAGTGGCTAGAATTCTTCTATCCACAGCTGAAGCCATGGGTTCACTAT  
ATCCAGTCAAAACAGATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAAT  
GATGATGTAGCTCAAGAGATTGCTGAAAGGGGAAGCCAGTTTATTAGGAACCATTTGCAG  
ATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATACTCTAAATTCCTGTCT  
TATAATGTAACGAGAAGGAAAGGTTATGATCAAATTTATCCCAAATGTTGAAAAC TGAA  
CTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCAACAGATCTCAGATATCCTAC  
GGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAAT  
ACCTGGTTTTTCCTTATCATGCTGCACCCAGAGCAACTCTTGAGAAAGATTTAAAATGTGT  
CTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGACCAGAAATCGTGAG  
ATGTGGATTTTGAACCCAACTCTACCTTTTCAATTTCTTAAGACCAATCACAGCTTGTGCC  
TCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATG  
CCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAACCTCATTGC  
TGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGGAAACCC  
TATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGGTAGC  
CATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAACCATAAACTCTGTTACTCAGGA  
GGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA



MEWWASSPLRLWLLFLFLPSAQGRQKESGSKWKVFIQINRSLENYEPSCSSQNCSCYHGV  
IEEDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFIVLEVIG  
RLPDMEMVINVRDYPQVPKWMPEAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPPIYPTG  
LGRWDLFREDLVRSAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQ  
AWKSMKDTLGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDWLEF  
FYPQLKPWVHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWE  
NLLSEYSKFLSYNVTRRKGYDQIIPKMLKTEL

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## FIGURE 137

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTG  
 CTGGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACCTACAGACGCTCCTGTTGGCTC  
 AGGACTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGA  
 GCAGTGCTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCAC  
 CTGCACCTTCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAA  
 GTTTCTTGTGAAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTC  
 CCGGAGCTGTACCAGGAACAGGAGGCACGTCTGTACCCATAAAAACCCAGGCTCCACT  
 GGCAGACGGCAGACAAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGA  
 ACTTCGGAGAGAAGCAACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGG  
 AGCCCAGCTGGGGATGGCCAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTC  
 CAGCTCCCCTTCCCGCTGAGAGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

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## FIGURE 138

MRPRCCILALVCWITVFLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAI  
LSLKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISR SCTRNR  
HVLYP

**Important features:**

**Signal sequence:**

amino acids 1-21

**N-myristoylation sites:**

amino acids 33-39, 70-76

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## FIGURE 139

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTC  
 TTGGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACA  
 ACAATGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATG  
 TTGACAATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCCTTG  
 CTGCAACCAGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCA  
 TGCCCTCCATTCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGAC  
 CAGGAGGACCACCTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACC  
 TGAGCAAGTTCGGAAAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTG  
 AGGAGATGCAAGAGGCAAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTAC  
 TATGGATTGTGGACATTTCTTCTGTGGAGACACGGTGGAGAACTTAAACAATTTTTTAAA  
 GCCACTATGGATTTAGTCATCTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTT  
 TTTACCATGTCATTCTGAAATTTTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAA  
 TAAAATCATTTAGCATTGAAAAAAA



GGTCTTAAATGGCAGCAGCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCC  
TGCTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCA  
CCGTCATCCCTAAGTTTACAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATG  
AAAAGACTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGG  
GGAAGAACTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGG  
TGGACATACTTACAGAGCAACTGCGTGACATTAGCTGGAGAATTACACACCCCAAGGAAC  
CCCTCACCCCTGCAGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGAT  
CTTGGCAGTTTCACTTTTCGATGGGCAGATCTTCCCTCCTCTTTGACTCAGAGAAGAGAATGT  
GGACAACGGTTTCATCCTGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTG  
TGGCCATGTCTTCCATTACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCT  
TGATGGGCATGGACAGCACCCCTGGAGCCAAGTGCAGGAGCACCACTCGCCATGTCCTCAG  
GCACAACCCAACTCAGGGCCACAGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCC  
TCCCCTGCTTTCATCCTCCCTGGCATCTGAGGAGAGTCCCTTTAGAGTGACAGGTTAAAGCT  
GATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAACCTCGCCCTTCTGTCTGCGCCAGC  
TGCCACACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGATCATGATGACATCATGGAC  
CCAATAGCTCATTCACTGCCTTGATTCCTTTTGCCACAACATTTTACCAGCAGTTATACCT  
AACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCACTTAAAGTTCTG  
GCTGACTAAACAAGATATATCATTTTCTTTCTTCTCTTTTTGTTTGGAAAATCAAGTACT  
TCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTGAGTAAATAATCACGTTAGAC  
TTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTTAAATTATTTAATAAG  
AAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA  
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 142

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKT  
FLHYDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLT  
LQARMSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAM  
SFHYFSMGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPC  
FILPGI

**Important features:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site:**

amino acids 68-72, 82-86

**N-myristoylation site:**

amino acids 200-206, 210-216

**Amidation site:**

amino acids 77-81

**FIGURE 143**

AATGTGAGAGGGGCTGATGGAAAGCTGATAGGCAGGACTGGAGTGTTAGCACACAGTACTGG  
ATGTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGC  
AAGGATCCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTG  
GCTTTCTCTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGG  
GATGCCCTGGGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCCTCCTACTCT  
CTGAGGCGCTGCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGC  
AGTAATGTGGACTGCCACCAAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCAT  
AATGATGTCAAGCACCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGAC  
AACCCATGTTCACTCAAGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCT  
AAGGTCTTAGATGGTACGCGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTA  
TGCCAAATTGTTGGCTGCGATCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGG  
GTCTGCAACGGAGATGGGTCCACCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTC  
TCCGCAACCAAATCGGATGATACTGTGGTTGCACTTCCCTATGGAAGTAGACATATTTCG  
CTTGCTTTAAAAGGTCCTGATCACTTATATCTGGAAACCAAACCCTCCAGGGGACTAAA  
GGTGAACACAGTCTCAGCTCCACAGGAACTTTCCTTGTGGACAATTCTAGTGTGGACTTC  
CAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTCACAGCAGATTTTCATT  
GTCAAGATTTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATCTTCTATCAACCC  
ATCATCCACCGATGGAGGGAGACGGATTTCTTTCCTTGCTCAGCAACCTGTGGAGGAGGT  
TATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCTGACCAA  
TACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAACTTG  
GATCCTTGTCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC  
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGGCATC  
CAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCATGTCACCTTCAGTGGA  
GAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTTGAC  
TGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTC  
AGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCA  
AAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAA  
GAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAA  
GGAGCTGCTGTGTGAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATATTTG  
AAACTGTTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGAAC  
TAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA  
AAAAAAAAA



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## FIGURE 144

MECCRATPGTLLFLAFLLLSSRTARSEEDRDGLWDAGPWSECSRTC GGASYS LRRL  
LSSKSEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCS  
LKCQAKGTTLVVELAPKVLDTGRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNG  
DGSTCRLVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDLHYLETKT LQGT KGENS  
LSSTGTFLVDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPI IHR  
WRETDFP CSATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCP  
ASDG YKQIMPYDLYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKC  
MYTPKMPIAQPCNIFDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKP  
HIKEECIVPTPCYKPKKLPVEAKLPWFKQAQAELEGA AVSEEPS

Important features:

Signal peptide:  
amino acids 1-25

N-glycosylation site:

amino acids 251-254

### Thrombospondin 1:

amino acids 385-399

von Willebrand factor type C domain proteins:

amino acids 385-399, 445-459 and 42-56

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## FIGURE 145

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCT  
CTCTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCCAGTCCCTGTA  
CGCCAAGGAACTGGTCCTGGGGGCACCAATGGTTTCGGCGGCAGCCCCCAGCCTCCTCATC  
CTTCTGTTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCGCTCTGTGCCCTGAAG  
GCCACGTTCCCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCC  
CCGAGCCTCCCGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCC  
ACAACCCTGGGGGGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTC  
CGCCAGTACGTGATGCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATC  
GTCTGTGCCGCGGTATCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCC  
TTCCCAAGAAGAAGTACGTGGACCAGAGTGACCGGGCCGGGGGCCCGGGCCTTCAGT  
GAGGTCCCCGACAGAGCCCCCGACAGCAGGCCCGAGGAAGCCCTGGATTCTCCTCCGGCAG  
CTCCAGGCCGACATCTTGCCCGCCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTG  
GGCGGTGGGGACGGAGCCAGGATGGTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGC  
AGCCAGGAGGGGGACCAGGAAGTCCAGGGACATGGGGTCCCAGTGGAGACACCAGAGGGC  
CAGGAGGAGCCGTGCTCAGGGGTCTTTGAGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGG  
GAGCTGGAAGGGTCTCTCTTGTAGCCAGGAAGCCAGGGACCAGTGGGTCCCCCGGAA  
AGCCCCCTGTGCTTGCAGCAGTGTCCACCCAGTGTCTTAACAGTCTCCTCCCGGGCTGCCAGC  
CCTGACTGTCCGGCCCCCAAGTGGTCACTCCTCCCGTGTATGAAAAGGCCTTCAGCCCTGA  
CTGCTTCCTGACACTCCCTCCTTGCCCTCCCTGTGGTGCCAATCCCAGCATGTGCTGATT  
CTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGAGGAATCTTACCAAGTGCCATCA  
TCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGCACAGCTCCCCTGACAAAGTG  
AGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCCCCCAAAGTGCTGGGATTA  
CAGGCGTGAGCCACCGTGCCCGGCCCAAACACTACTTTTTTAAACAGCTACAGGGTAAAATC  
CTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCTGAAGGTGGCCCCCTGTTTC  
TAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTCTCAAGCGCTCTC  
CAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGGGATCAGGTTG  
AATGAATGGAACCTCTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGGGCTGTGTT  
TGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACGCCCAGC  
CTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTGTGTC  
CACAATATTTCGTACGTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCTCT  
GGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAA  
AAGA

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## FIGURE 146

MVSAAAPSLILLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTP  
ALSPTSMGPQPTTLGGPSPPTNFLDGIVDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQ  
KQKASAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRP EEALDSSRQLQADILAA  
QNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVL  
EGAVVAGEGQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site:**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

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## FIGURE 147

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTG  
 CTGCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGA  
 AGGAACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGAC  
 AAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTC  
 TTGGAGAATTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTA  
 TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATT  
 AATACATTTACTATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAC  
 GAAAAGGATGGGGAAACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGT  
 TCAGACATCAAGGAAAGGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAAT  
 ATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCCGAGAATGAAGAATGGCCTGA  
 GCCTCCAGTGTTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCAT  
 ACAGCATCCCCAGTATAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCA  
 ATTCCAGTCTATCAACATGTTACCTAGGATACCTCATCAAGAATCAAAGACTTCTTTAAA  
 TTTCTCTTTGATACACCCTTGACAATTTTTCATGAAATTATTCCTCTTCCTGTTCAATAA  
 ATGATTACCCTTGCACTTAA

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFL  
 EQIHVLENSLVLKVHTVRDEECSELSMVAADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLM  
 AHLNEKDGETFQLMGLYGREPDLS DIKERFAQLCEEHGILRENIIDL SNANRCLQARE



Cell attachment sequence:  
amino acids 301-304

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## FIGURE 151

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACC  
TCGTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTG  
CTGTTCCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATG  
CTCGTGCTCCTGCTGGACTTTCTTGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCAC  
ATCTACCTGAGTATGTCCCCACCCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTTCAGA  
GCTGCTCATCTTACACCTCTACTTGAGTATGTCCCTAACCCCTGAGCCCCCAGCCTGGG  
GCCAGAGTCTTTGTCCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAAGTGAG  
ATCATGGACAAAAAGGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCC  
CAGCAAGAAGCTGAACTCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAAC  
AAGTTTAAAATGTTTCAGAGACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATG  
AAATAAGGACAGGTGGACTTCCAAAAACACAAGTAGAAATTCTAACAATGAAATATATTA  
CAGGCAGGTCACCCACTAACCAAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCA  
CAGTGGGCACAGCGGTAGGCGGTGAGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCA  
GCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCCCTGCTCCTGGCACCAGCCGTT  
TTGGTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTGGGCAGTGGTGGCCCCGAG  
GCTGTGGCCTCTCAGGGGGTTTCTGTGGACACGGGCAGCAGAGTGTGTCCAGGCCAGCCC  
CCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCAGAGGGAGTTGGG  
TGGGTCAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCTGCCTGCAGTTGTGGCAA  
GAACGCCCAGCTCAGAATGAACACACCCCAACCAAGAGCCTCCTTGTTTCATAACACAGGT  
TACCCTACAAACCACTGTCCCCACACAACCCCTGGGGATGTTTTAAAACACACACCTCTAA  
CGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC  
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA



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## FIGURE 152

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQ  
GWVVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSM  
RTQQAQQEAELTPRPAGVVPGA

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## FIGURE 153

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCC  
TGTCTTTATGTCTTTCTCCTCTTCCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCT  
GTCAGCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAA  
CCTATGTTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGT  
GCTTCTGTGATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAA  
ATCTGGCATGAGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTAT  
TCCTCCTCCCAAGTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGG  
CATTACAGAGAAAGCAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGA  
AATGGAGGAGCTTTGTAGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCT  
GCCCCGCCGTAGATTTCAGGACATTTCGCCCCGTGTGTGCCACCAAACCAGGACTTTCCCCTT  
GGCTTGGCATCCCTGGCTCTCTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTA  
GCATCTTTCAAGCTCCGTTACTATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGA  
ATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGT  
TCTCCCTACCCTGAGGAAAAACCAAAGGGAAGCAACAGGAACTTCTGCAACTGGTTTTTA  
TCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCACAAGAAATGTAGCTGGAGA  
AGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCTGGGAGTCAGACCTGG  
AATTCTGATTCCAAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCCCCGTAGCCATCT  
CCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAACTAACAATGTAGGTT  
ACTAGTGAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAA  
AATTCTCTAACACTGAAA

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## FIGURE 154

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGS  
MEHRNHLCFCDLYDRATSPPLKCSLL

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## FIGURE 156

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTD  
AMSNACKELAIFLTGTIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVF  
GSNDDFSWQQW

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# FIGURE 157

GTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCG  
 GGAGCGACGCAGCTTGAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAG  
 CCGAGTGGCCCGAGGTGTCTGAGGGGCTGGGGCAAAGGTGAAAGAGTTTCAGAACAAAGCT  
 TCCTGGAACCCATGACCCATGAAGTCTTGTCGACATTTATACCGTCTGAGGGTAGCAGCT  
 CGAAACTAGAAGAAGTGGAGTGTTGCCAGGGACGGCAGTATCTCTTTGTGTGACCCTGGC  
 GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACG  
 GCGTGGAGAGGAATGAGGCCTGAGGTCACACTGGCTTGCTCCTCCTAGCCACAGCAGGC  
 TGCTTTGCTGACTTGAACGAGGTCCCTCAGGTCACCGTCCAGCCTGCGTCCACCGTCCAG  
 AAGCCCGGAGGCACCTGTGATCTTGGGCTGCGTGGTGGAAACCTCCAAGGATGAATGTAACC  
 TGGCGCCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCCTCATCACC  
 CACGGGACCCCTCGTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAGTGTGTG  
 GCCCCGATGCCTGCGGGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTC  
 CAGGACTTCAAGTTAGATGTGACGACGTTGATGAAGTGGATGAGGGAAACACAGCAGTC  
 ATTGCCTGCCACCTGCCTGAGAGCCACCCCAAAGCCCAGGTCCGGTACAGCGTCAAACAA  
 GAGTGGCTGGAGGCCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCTACAACCCAGTGACC  
 CAGGAAGTGAAAACCTCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAG  
 GCTGCCCCGCATCATCTACCCCCCAGAGGCCCAAACCATCATCGTCACCAAAGGCCAGAGT  
 CTCATTCTGGAGTGTGTGGCCAGTGGAAATCCCACCCCCACGGGTACCTGGGCCAAGGAT  
 GGGTCCAGTGTACCCGGCTACAACAAGACGCGCTTCCTGCTGAGCAACCTCCTCATCGAC  
 ACCACCAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAG  
 CCCGGGGCAGCGGTATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATG  
 GAGCTATCCAGCTGGTTCATCCCTGGGGCCAGAGTGCCAAAGCTTACCTGTGAGTGTGCT  
 GGGAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCCCCCTCATCTCCAGCCAG  
 CGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGCTCAGCATGGGGCCTGAGGACGAAGGC  
 GTCTACCAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGG  
 ACCTCCAGGCCAAGCATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACA  
 CCTCCTGTATCACCCCTCCAACTCGGCAACCTGAGCAGATGCTGAGGGGGCAACCGGCG  
 CTCCCCAGACCCCCAACGTCAGTGGGGCCTGCTTCCCCGAAGTGTCCAGGAGAGAAGGGG  
 CAGGGGGCTCCCCCGAGGCTCCCATCATCCTCAGCTCGCCCCGACCTCAAGACAGAG  
 TCATATGAACTGGTGTGGCGGCCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTAC  
 TATGTGGTGAAACACCGCAAGCAGGTCAAAATTCTCTGACGATTGGACCATCTCTGGC  
 ATTCCAGCCAACAGCACCGCCTGACCCTCACCAGACTTGACCCCGGGAGCTTGTATGAA  
 GTGGAGATGGCAGCTTACAACCTGTGCGGGAGAGGGCCAGACAGCCATGGTCACCTTCCGA  
 ACTGGACGGCGGCCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC  
 GACCCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCACGGCCGCCTCTCCCCCCCA  
 GAAGCTCCCGACAGGCCCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGG  
 ATTCCCCGTGGGAATGGTGGGTTCCCAATCCAGTCCTTCCGTGTGGAGTACAAGAAGCTA  
 AAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCATCGCGGCTGTCCGTG  
 GAGATCACGGGCCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG  
 CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGGCTACAGCGGT  
 CGCGTGTACGAGAGGCCCCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAATGAG  
 ACCACCATCATGCTCAAGTGGATGTACATCCCAGCAAGTAACAACAACACCCCAATCCAT  
 GGCTTTTATATCTATTATCGACCCACAGACAGTGACAATGATAGTGACTACAAGAAGGAT  
 ATGGTGAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC  
 GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCGAGTTTCAGCAACGTGATGATC  
 TGTGAGACCAAAGCTCGGAAGTCTTCTGGCCAGCCTGGTTCGACTGCCACCCCCAACTCTG  
 GCCCCACCACAGCCGCCCCCTTCTGAAACCATAGAGCGGCGGCTGGGCACTGGGGCCATG  
 GTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGGTCGTCCTGGGCTCCATCGTT  
 CTCATCATCGTCACCTTCATCCCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT  
 ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCCTCCTGCCCCGTATACTATGGTG  
 CCATTGGGAGGACTCCCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGT

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GGACGGGCCTGTGCTAATGGGATCCACATGAATAGGGGCTGCCCCTCGGCTGCAGTGGGC  
TACCCGGGCATGAAGCCCCAGCAGCACTGCCCAGGCGAGCTTCAGCAGCAGAGTGACACC  
AGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCACCAGATC  
ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGGCTCTTTCTTATACACACTGCCCCGACGAC  
TCCACTCACCAGCTGCTGCAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCT  
GCTGTGGGCCAGTCAGGGGTGAGGAGAGCCCCCGACAGTCCTGTCCTGGAAGCAGTGTGG  
GACCCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCCTTGTGCCAGTTGAAGAGGTG  
GACAGTCCTGACTCCTGCCAAGTGAGTGAGGAGAGACTGGTGTCCCCAGCACCCCGTAGGG  
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCACTGGTGCGTGTGTCT  
TTTGAAACACCACCTCTCACAATTTAGGCAGAAAGCTGATATCCCAGAAAAGACTATATATT  
GTTTTTTTTTTTAAAAAAGAAAGAGACAGAGAAAATTGGTATTTATTTTTC  
TATTATAGCCATATTTATATATTTATGCACTTGTAATAAATGTATATGTTTTATAATTC  
TGGAGAGACATAAGGAGTCCTACCCGTTGAGGTTGGAGAGGGAAAATAAAGAAGCTGCCA  
CCTAACAGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCT  
GGGGCCTCTGCAGTGGCAGGCGAGGCTGCAGGAGGCCCCACAGATAAGCTGGCAAGAGGAA  
GGATCCCAGGCACATGGTTCATCACGAGCATGAGGGAACAGCAAGGGGCACGGTATCACA  
GCCTGGAGACACCCACACAGATGGCTGGATCCGGTGCTACGGGAAACATTTTCCTAAGAT  
GCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAAAAACCTTCCAGAAT  
CAATAATCCGTGGCAACATATCTCTGTAAAAACAAACACTGTAACCTTCTAAATAAATGTT  
TAGTCTTCCCTGTAAAA





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GACCATAGAAAGCTATGTTCTTACTTTGTGTGTGTGTCTGTATGTTTCTGCGTTGTGTGT  
CTTTGTAGGCAAGCAAACGTTGTCTACACAAACGGGAATTTAGCTCACATCATTTTCATGC  
CCCTGTGCCTCTAGCTCTGGAGATTGGTGGGGGGAGGTGGGGGGAAACGGCAGGAATAAG  
GGAAAGTGGTAGTTTTAACTAAGGTTTTGTAACTTGAATCTTTTCTTCTCAAATTA  
ATTATCTTTAAGCTTCAAGAACTTGCTCTGACCCCTCTAAGCAAACCTACTAAGCATTTA  
AAAGAGAATCTAATTTTTAAAGGTGTAGCACCTTTTTTTTTTATTCTTCCCACAGAGGGTG  
CTAATCTCATTATGCTGTGCTATCTGAAAAGAACTTAAGGCCACAATTCACGTCTCGTCC  
TGGGCATTGTGATGGATTGACCCTCCATTTGCAGTACCTTCCCAGCTGATTAAAGTTCAG  
CAGTGGTATTGAGGTTTTTCGAATATTTATATAGAAAAAAAGTCTTTTCACATGACAAAT  
GACACTCTCACACCAGTCTTAGCCCTAGTAGTTTTTTTAGGTTGGACCAGAGGAAGCAGGT  
TAAATGAGACCTGTCTCTGCTGCACTCAGAAAAAATAGGCAGTCCCTGATGCTCAGATC  
TTAGCCTTGATATTAATAGTTGAGACCACCTACCCACAATGCAGCCTATACTCCCAAGAC  
TACAAAGTTACCATCGCAAAGGAAAGGTTATTCCAGTAAAAGGAAATAGTTTTCTCAACC  
ATTTAAAAATATTCTTCTGAACTCATCAAAGTAGAAGAGCCCCCAACCTTTTCTCTCTGC  
CTTCAAGAAGGCAGACATTTGGTATGATTTAGCATCAACAACACATTTATGAGTATATGT  
AAGTAATCAGAGGGGGCAAATGCCACTTGTTATTCCCTCCCAAGTTTTCCAAGCAAGTACAC  
ACAGATCTCTGGTAGGATTAGGGGGCCACTTGTGTTTTCCGGCTTATTTTAGTCGACTTGTCT  
AGCAAGTTTGATGCCTAGTCTATCTGACATGGCCCAGTAGAACAGGGCATTGATGGATCA  
CATGAGATGGTAGAAGGAACATCATCACATAACCCCTCTCACAGAGAAAATTATCAAAGAA  
CCAGAAATTATATCTGTTTTTGGAGCAAGAGTGTCATAATGTTTCAGGGTAGTCAAATAA  
ACATAAATTATCTCCTCTAGATGAGTGGCGATGTTGGCTGATTTGGGTCTGCCATTGACA  
GAATGTCAAATAAAAAGGAATTAGCTAGAATATGACCATTAAATGTGCTTCTGAAATATA  
TTTTGAGATAGGTTTAGAATGTCA

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## FIGURE 160

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEA  
PHNLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTL  
SSNQITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI  
FQDCRSKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLLSLHSLCL  
RRNKVAIVVSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRITYIEPRIL  
NSWKSLSITLAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAF  
HLCEDGAEP TSGHLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAE  
NAVQIHKVVTGTMALIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQM  
AAMSAQEYYVDYKPNHIEGALVIINEYGSCTCHQQPARECEV



amino acids 68-340

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## FIGURE 163

CAGAGAGGAGGCTTTGGGAATTGTCCAGCAGAAACAGAGAAGTCTGAGGTGGTGTCAAGA  
 CAAAAGATGCCTTCAGCTTTGGAAACTTGTTCTCCTGTGCGGCGTGCTCACTGGGACCTCA  
 GAGTCTCTTCTTGACAATCTTGGCAATGACCTAAGCAATGTCGTGGATAAGCTGGAACCT  
 GTTCTTCACGAGGGACTTGAGACAGTTGACAATACTCTTAAAGGCATCCTTGAGAACTG  
 AAGGTCGACCTAGGAGTGCTTCAGAAATCCAGTGCTTGGCAACTGGCCAAGCAGAAGGCC  
 CAGGAAGCTGAGAAATTGCTGAACAATGTCATTTCTAAGCTGCTTCCAACCTAACACGGAC  
 ATTTTTGGGTTGAAAATCAGCAACTCCCTCATCCTGGATGTCAAAGCTGAACCGATCGAT  
 GATGGCAAAGGCCTTAACCTGAGCTTCCCTGTCACCGCGAATGTCACTGTGGCCGGGCCC  
 ATCATTGGCCAGATTATCAACCTGAAAGCCTCCTTGGACCTCCTGACCGCAGTCACAATT  
 GAAACTGATCCCCAGACACACCAGCCTGTTGCCGTCCTGGGAGAATGCGCCAGTGACCCA  
 ACCAGCATCTCACTTTCCCTTGCTGGACAAACACAGCCAAATCATCAACAAGTTCGTGAAT  
 AGCGTGATCAACACGCTGAAAAGCACTGTATCCTCCCTGCTGCAGAAGGAGATATGTCCA  
 CTGATCCGCATCTTCATCCACTCCCTGGATGTGAATGTCATTCAGCAGGTCGTCGATAAT  
 CCTCAGCACAAAACCCAGCTGCAAACCCTCATCTGAAGAGGACGAATGAGGAGGACCACT  
 GTGGTGATGCTGATTGGTTCCCAGTGGCTTGCCCCACCCCCTTATAGCATCTCCCTCCA  
 GGAAGCTGCTGCCACCACCTAACCAGCGTGAAAGCCTGAGTCCCACCAGAAGGACCTTCC  
 CAGATACCCCTTCTCCTCACAGTCAGAACAGCAGCCTCTACACATGTTGTCTGCCCCCTG  
 GCAATAAAGGCCCATTTCTGCACCCTTAA

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## FIGURE 164

MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNNTLKGILEKLKV  
DLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLIILDVKAEPIDDG  
KGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIETDPQTHQPVAVLGECASDPTS  
ISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQ  
HKTQLQTLI

### Important features:

#### Signal peptide:

1-15

#### Transmembrane domain:

none

#### N-glycosylation site:

124-128, 132-136

#### N-myristoylation site:

12-18, 16-22, 26-32, 101-107, 122-128, 141-147

#### Leucine zipper pattern:

44-66

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## FIGURE 165

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTGTAGTGC  
CTTGCTTCCTGAACTAGCTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCA  
CTCTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGG  
ATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATC  
CAGAGCCCCGCGGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA  
CCCTGCTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGT  
TTCAGTACTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGAT  
TAGGAAATACGTCCCAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAA  
GTCTGCAGCATGTGGCTGAAAACTCTGTGCTGAGCTGTATAACAAAGCTGGAGCACACA  
GGTGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATA  
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGC  
TGAAGATAAACAAACAAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTT  
TCTACTCTTATTGGACAGGGCTTTTGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGG  
ATGGAACCCCTTTCACCTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAA  
GCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGA  
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCC  
CTGAAACATTAGGCGAAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGC  
CAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAG  
ACTATCTCTCTGACTAGTACAAAATGGGTCTCGTGTTTCTGTTTCTGTTTCTGTTTCTGTTT  
TTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCAC  
CAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC  
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCTTACACTTGGT  
GGAATAAGAACTTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACA  
GTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAG  
GAATTCTTTTTTGTGTTTGTTCAGTTTCTACTAGTCCCTTCCCAATCCATCAGTAAAGACCC  
CATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACCTTGATATGAGAATCTCAAAT  
CTCAATGCCTTATAAGCATTCCTTCCCTGTGTCCATTAAAGACTCTGATAATTGTCTCCCCT  
CCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTTCATATCAGAACTAC  
CGTCCCCGATATTCCTTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTG  
CACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGT  
ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA



MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRTEHRAPSSTWRPVALTLLTLCLV  
LLIGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEK  
LCRELYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQED  
LEFAASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSRPSRDCVAIL  
NGMIFSKDCKELKRCVCERRAGMVKPESLHVPPETLGED

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## FIGURE 167

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCC  
 CTCAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA  
 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC  
 GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT  
 GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT  
 GTGGGTTCGTTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT  
 GACATAGGACCCCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG  
 CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC  
 ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG  
 GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGC  
 ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG  
 GCCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC  
 CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC  
 GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC  
 ACCATGTACTTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC  
 CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC  
 CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT  
 AAAC TGAGAAAATGGCCTATGCTTAAGAGGAAAATGAAAGTGTTCCTGGGGTGCTGTCTC  
 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC  
 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATACAATAAAATCTTTAAG  
 TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 168

MRGNLALVGVLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR  
VGPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRK  
AIGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP  
KDEAANGLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEE  
DCVEMVASGGWNDVACHTTMYFMCEFDKENM

FIGURE 169

AGTGACTGCAGCCTTCCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGC  
AGCACCAAGTGTGTGAGGGGAGCAGGCAGCGGTCTTAGCCAGTTCCTTGATCCTGCCAGAC  
CACCCAGCCCCCGGCACAGAGCTGCTCCACAGGCACCAATGAGGATCATGCTGCTATTAC  
AGCCATCCTGGCCTTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGA  
GGAGGTGGTTCTTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCA  
GAGACTCTTCAAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAG  
CACAGATCCTAAGGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGG  
ACTTATGGGCAAGAGGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGT  
GAGGGTTCTCTCGGCCCTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGG  
AACAGAGGAGCAGAGACCTTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCC  
CAGCTTTGGCATCCTCAAGTATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCC  
TGGACTGCATTAGGAAGACCTCTTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTT  
ACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTC  
TACCTGACCCTGGTGTGGAAACTGCATAGTGAATATCCCCAACCCCAATGGGCATTGACT  
GTAGAATAACCTAGAGTTCTGTAGTGTCTACATTAAAAATATAATGTCTCTCTCTATT  
CCTCAACAATAAAGGATTTTTTGCATATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA



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## FIGURE 172

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEEC  
HPGSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Signal peptide:**  
amino acids 1-19

**Tyrosine kinase phosphorylation site:**  
amino acids 88-95

**N-myristoylation sites:**  
amino acids 33-39, 35-41, 46-52

# FIGURE 173

AGCGCCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAA**TGT**CTT  
TCCTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGG  
GGGCTGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGA  
AAGCGGCCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGA  
CTTTCAAAGCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGC  
CAGGCTGTTTCCTCTGTGCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGG  
ACCAGCTGGGCGTCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGG  
ATTTCCAGCCTTATTTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTC  
CACAAAGGCGGAAGATGATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCT  
TCCGAGCCTGGAACGGAGGCTTCTCTGGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGG  
GAGTTTTTCGTGGTGGGATCAGGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAAT  
TTGGAGACAAAGTAAACCTACTTTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGA  
CTTTGGCCTCAGAGAAAAAA**TGA**TTGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGAC  
ATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCC  
ATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAATATTCTGTTTAGGCCAC  
TAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAACTAATGAGGATTATT  
AAGCTAAAACCTGGGAAATAGGAGGCTTAAATTTGACTGCCAGGCTGGGTGCAGTGGCTC  
ACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAGGTGCGGAGT  
TCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAAATCACC  
CGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAATCA  
CTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG  
GGTGA CTGAGACTCTAACTAA



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## FIGURE 174

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKE  
PRTFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTE  
VKDFQPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFI  
LGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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## FIGURE 176

MAPLALHLLVLVPILLSLVLASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQ  
RVIVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSS  
HRILHKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPE  
DIYQMALNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEDGFFY  
LSFAEALRAHSCLSDRLQYSRIVGGWDLPLRALLSSLSGLVLLNAPVVAMTQGPHDVHVQ  
IETSPPARNLKVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFR  
RPFWREEHIEGGHSNTDRPSRMIFYPPPREGALLASYTWSDAFAAGLSREEALRLAL  
DDVAALHGPVVRQLWDGTGVVWRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAG  
EHTAYPHGWVETAVKSALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHD  
LAKEEGSHPPVQGGQLSLQNTTHTRTSH

**Signal peptide:**  
amino acids 1-21

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## FIGURE 177

CCGGGGAGGGGAGGGCCCGTCCCGCCCCCTCCCCGTCTCTCCCCGCCCCCTCCCCGTCCCTC  
 CCGCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGGCTGC  
 CCTCTGCCCCGGGTGTCCAAGATGGAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGGCTC  
 CTGCTGTTTCGTGGCGCTACCCGCCTCCGGCTGGCTGACGACGGGCGCCCCCGAGCCGCCG  
 CCGCTGTCCGGAGCCCCACAGGACGGCATCAGAATTAATGTAACCTACACTGAAAGATGAT  
 GGGGACATATCTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTAT  
 GTAAATGACTTACCTGTAAATAGTGGTGTAACCCGAATAAGCTGTCAGACTTTGATAGTG  
 AAGAATGAAAATCTTGAAAATTTGGAGGAAAAAGAATATTTTGGAATTGTCAGTGTAAGG  
 ATTTTAGTTCATGAGTGGCCTATGACATCTGGTTCAGTTTGCAACTAATTGTCATTCAA  
 GAAGAGGTAGTAGAGATTGATGGAAAACAAGTTCAGCAAAAGGATGTCACTGAAATTGAT  
 ATTTTAGTTAAGAACCGGGGAGTACTCAGACATTCAAACCTATACCCCTCCCTTTGGAAGAA  
 AGCATGCTCTACTCTATTTCTCGAGACAGTGACATTTTATTTACCCCTTCCTAACCTCTCC  
 AAAAAAGAAAGTGTTAGTTCACTGCAAACCACTAGCCAGTATCTTATCAGGAATGTGGAA  
 ACCACTGTAGATGAAGATGTTTTACCTGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAG  
 CCGCCATCTTCATATAAGGTAATGTGTGAGTGGATGGAAAAGTTTAGAAAAGATCTGTGT  
 AGGTTCTGGAGCAACGTTTTTCCCAGTATTCTTTTCAAGTTTTTGAACATCATGGTGGTTGGA  
 ATTACAGGAGCAGCTGTGGTAATAACCATCTTAAAGGTGTTTTTCCCAGTTTCTGAATAC  
 AAAGGAATTCTTCAGTTGGATAAAGTGGACGTCATACCTGTGACAGCTATCAACTTATAT  
 CCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAAGATAAAACATGTATTTAAAACGCC  
 ATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCCAAATTTGCCACTTGAATATAAT  
 TTTCTTTAAATCGTT

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## FIGURE 178

MEGAPPGSLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQ  
VVLNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWP  
MTSGSSLQLIVIQEEVVEIDGKQVQKQDVTEIDILVKNRGVLRHSNYTLPLEESMLYSIS  
RDS DILFTLPNLSKKESVSSLQTTSQYLIRNVETTVDVLPGLPETPLRAEPPSSYKV  
MCQWMEKFRKDLCRFWSNVFPVFFQFLNIMVVGITGAAVVITILKVFFPVSEYKGILQLD  
KVDVIPVTAINLYPDGPEKRAENLEDKTCI

**Signal peptide:**

1-23

**Transmembrane domain:**

266-284

**Leucine zipper pattern:**

155-177

**N-glycosylation site:**

46-50, 64-68, 166-170, 191-195

**Motif name: N-myristoylation site:**

3-9, 42-48, 273-279

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## FIGURE 179

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATAC  
 GTCCCCGGGCAGGGGTGACAACAGGTGTCATCTTTTGGATCTCGTGTGTGGCTGCCTTCC  
 TATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTC  
 CTAACCTTCCCTTCTTGAACCCCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAA  
 CCAGCAAGCGGCTCCTTTCGGCTTAACTTGTGGTTGGAGGAGAGAAACCTTTGTGGGGCTGC  
 GTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGAAAGGT  
 CCCCTCTTGCTGTTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAAGGTGAAAACCTTG  
 GAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAAAGTAGAGAAGCT  
 GCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAG  
 CAGCTCCGGGGGGCCCCAAACGCATGCTTCCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTG  
 GGGGCCCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCTGAATGATG  
 ATGGTTTCGCCGGGGGGCTGCTTGCGTGGATTTCCCGGGTGGTGGTTTTGCTGGTGCTCCTC  
 TGCTGTGCTATCTCTGTCTGTACATGTTGGCTGCACCCCAAAGGTGACGAGGAGCAG  
 CTGGCACTGCCCAGGGCCAACAGCCCCACGGGGAAGGAGGGGTACCAGGCCGTCCTTCAG  
 GAGTGGGAGGAGCAGCACCGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTC  
 AAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAATGGGCAGTACCAAGCCAGCGAT  
 GCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTCCTGGCC  
 TTCCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAG  
 TATGCAGCAGTGCCCTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGC  
 CTTACCCGCCACCCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAA  
 GCCATTGAATCAGCCTTGGAGACCCTGAACAATCCTGCAGAGAAACAGCCCCCAATCACCGT  
 CCTTACACGGCCTCTGATTTTCATAGAAGGATCTACCGAACAGAAAGGGACAAGGGGACA  
 TTGTATGAGCTCACCTTCAAAGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTT  
 CGACCATTACAGCCCCATCATGAAAGTGAAAAATGAAAAGCTCAACATGGCCAACACGCTT  
 ATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAGTTCCGGCAGTTCATGCAGAAT  
 TTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG  
 AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAAGCTGCCAACTTC  
 AGGAACCTTTACCTTTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTGATGTT  
 GGAGCCCCGCTTCTGGAAGGGAAGCAACGTCCTTCTCTTTTTCTGTGATGTGGACATCTAC  
 TTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAGGTATTT  
 TATCCAGTTCCTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTC  
 CCTCCCTTGGAACAGCAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGA  
 TTTGGGATGACGTGTCAGTATCGGTGAGACTTCATCAATATAGGTGGGTTTGATCTGGAC  
 ATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTCCACAGCAACCTC  
 ATAGTGGTACGGACGCCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATG  
 GACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCA  
 TCCCACGGCCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAA  
 CAGAAACAGAAGACAAGTAGCAAAAAAACATGAACTCCCAGAGAAGGATTGTGGGAGACA  
 CTTTTTCTTTCTTTTGGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
 GGACGACAAAAGAATTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGT  
 TGGGCTTTTTTACAACAGAAATCAAATCTCCGCTTTGCCTGCAAAAGTAACCCAGTTGCA  
 CCCTGTGAAGTGTCTGACAAAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTGTGGA  
 GGTTTTGATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGAAATATT  
 CATGATTTAAGAGCAGTTTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCC  
 TCATATGAATGAGCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGG  
 CAGGAGAGGAGATAGGCTTATTATGATACTAGTGAGTACATTAAGTAAATAAAATGGAC  
 CAGAAAAGAAAAGAAACCATAAATATCGTGTCAATTTTCCCCAAGATTAACCAAAAATA

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ATCTGCTTATCTTTTTGGTTGTCCTTTTAACTGTCTCCGTTTTTTTTCTTTTATTTAAAAA  
TGCACCTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTT  
ACAAGAGAGCACAAAGTTGGCCTACATTTTTTATATTTTTTAAAGAAGATACTTTGAGATGCA  
TTATGAGAACTTTTCAGTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATG  
CTGATTCTGTCAGGCACTGAATGTCAGGCATTGAGACATAGGGAAGGAATGGTTTTGTACT  
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACT  
GGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGA  
TATCGTGATGTACCTAAAAGTCAGAAACCACATTTTCTCCTCAGAAGTAGGGACCGCTTT  
CTTACCTGTTTTAAATAAACCAAAGTATACCGTGTGAACCAAACAATCTCTTTTCAAACA  
GGGTGCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATATATATA  
TATATATATTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGCT  
ACATGTTATCCACCCCAGGCCAGGTGGAAGTAACTGAATTATTTTTTAAATTAAGCAGTT  
CTACTCAATCACCAAGATGCTTCTGAAAATTGCATTTTATTACCATTTCAAACATTTTTT  
TAAAAATAAATACAGTTAACATAGAGTGGTTTCTTCATTCATGTGAAAATTATTAGCCAG  
CACCAGATGCATGAGCTAATTATCTCTTTGAGTCCTTGCTTCTGTTTGCTCACAGTAAAC  
TCATTGTTTTAAAAGCTTCAAGAACATTCAAGCTGTTGGTGTGTTAAAAAATGCATTGTAT  
TGATTTGTACTGGTAGTTTATGAAATTTAATTAAAAACACAGGCCATGAATGGAAGGTGGT  
ATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

## FIGURE 180

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV  
 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADL  
 LAFLHSQVDKAEVNAGVKLATEYA AVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDEL  
 VEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI  
 LFRPFSPIMKVKNEKLN MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY  
 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD  
 IYFTSEFLNTCRLNTQPGKKVFYPVLF SQYNPGIIYGHHD AVPPLEQQLVIKKETGFWRD  
 FGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLI VVRTPVRGLFHLWHEKR  
 CMDELTPEQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT





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## FIGURE 182

MRPGAPGPLWPLPWGALAWAVGVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRAE  
CCASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCE  
CAPDCSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEHVVCPRPQ  
SCVVDQTGSAHCVVCRAAPCPVPSSPGQELCGNNNVITYISSCHMRQATCFLGRSIGVRHA  
GSCAGTPEEPPGGESAEEEEENFV

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites:**

amino acids 73-77, 215-219

**Osteonectin domain proteins:**

amino acids 97-130, 169-202

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## FIGURE 183

CACTCATTTCATTCCAAAGGGTCTCTCAAGGCAATGGTAATGTGCAAGGAGGTGATACCTA  
AATGAATGACCAAAAGAACATGCTTCTGCTTTTGTGTGTCTCCTACATTTTAGACATTTG  
TTTGTTTCTCTTGGTAGCCTTTAAATTCCTTGAAGCCCAGGACCATGTCTCACTTACCTT  
TGTGTTTCCACTAACTAGTCTACCTCCTGGAATTGGCAGATACTCAGTGAAAGCCTGTGA  
AATAAGTGATGTCTATTTCTAGCATATTATTCTGAGATTTAATGATAGATTTAGTGATTG  
AATGAGATTTCCATTTTCAAATACAGCAAAAGCATAACTATTTTCATTTCATTTCATATTCA  
TTCAACTTCATTCTCAAAATTAGGTCTGAGTTAACTAATAATTACCTTTGAAATGTGTG  
GGTTATTTGAGGCAATCAGGTGGTGACATTGAGCTCTCAGCCAGAGTTTGTCTTGGAAT  
TGATTTCAGTTCCATTGCATTGATTTTGTCTCAGAAGCCAAGGTTCCCATGAAAAATC  
ATTCCCACTTGAATTGGGCTGTGATTCTTGCTGCGTTTAAGTAAAGGAAGCCTCTTGTT  
CTAGTTCTGCAAACCTTACACACTGAACTGGGACAAGTTTTTGTCTTAGAGTAATGGCTGGG  
AAAAGAGGAACCTTTTCATTTTATTTCAGAAGTCAAAAACAAAGGCCTCCAGCCACCTGGA  
GATGTTTTGTTGCAGACACCAGCCTGGCTCTGTCTTTATGCCTAACAAATTGAGCATCCAG  
TCTTCTTTGTGCTGGGACCATTGCTCAGCTCTGCAAGGGGAAAAGAGGGAGAAAGCCAGA  
GCTGCCAGGCTTCTTGCACTGGGGCCGGGGGAGGGTTCTTGGAAGCAGGTGCTCTCTG  
CTTCTTGGTACGTGAGGCTCTCGGAGCTGCCTCTCCTCTGACCCTCAGGTCCTCACCGAG  
TTTGCTCCAGGAGTATATTGAAAACATACCCAGTGCTCTCTCAAGCACCCACTGCTTAGA  
GGGCCCAGATTTCTTTTCCTTCTTTCCCTTGCAAGCTGGAGACTGCATCGGGCATCTGG  
TGTTTAAACTAAACAGGAAAACCTGACTAAAGGTCCACAGTGCTCATTGTGTAGACTAGCT  
GCCCTCCGATGGGTGCTCTGATTATCAGTGTTCCAGTGCAAGGCCTGTCACCTAAACAGG  
CCTCACTTCCTCCTTGGGGGCTTTCCCATGGGAGGTGTGGCTTTTTACTCTACATGGAAA  
TGACTCTCTGCAGCCACAGAACACAGTCATTTTCTGAATTATCCAGTCTCTCATGCGCC  
CTGGATTCTCCAGATGCCTTATATCTCTTGTGCAAAGTTGTCTAAAATTTGGTTCCAG  
CTTCCAAGCCTTGCCCTTTTGGCCTTCCTGGAAGTATTTTTGTTGATGAGTCGTCTGTCAT  
TATTCTCTAAAATGATTTGCTTTTTTGTCTTTTCATTTCCTATTTCCACCCCACATATACA  
CACATGCTTCTTAACTTAGGGGATTACATGCCAATAAATCTATTGTTGAAAATGCACTAA  
TACTATCGCAAAGACGAAAATTCACAGGCTGAACCGTTGTAAGTCCATATGCTCCTCAAC  
TTACATGTGTGATGGAGTTATGCCCAAATAAGTCCATCGTCAAGTTGAAAAATCAAATC  
AAGCCATCTTAGGTTGAGGACCATTGTGTTGTACCTCCAAAGATGTCATATCTTTAAACA  
TACTCCCTAGCTTTTCTTTTACTTTTTATTTTGAAGTAATTATAGAATCACAGAAAGTT  
GCAAAAAA



## FIGURE 185

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCCA  
GGGTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC  
ATGTATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCT  
CTTTGGCCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGG  
ACAGATGCTCGGTAAATGCACTTTCTCCAGCTTTGCCCCCTGTGGGTGATGCTCTAACA  
GTGACCTGGAATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCAC  
ATAGATCCCTTCCAACCCATGAGTGGGCGGTTTAAGGACCGGGTGCTTGGGATGGGAAT  
CCTGAGCGGTACGATGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACA  
TACACCTGCCAGGTGAAGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTC  
AGCGTCGTGCACACTGTACGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCT  
GCCTGTGCACTGATGATCATAATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAA  
AAGCGATGGGCCGAAAGAGCTCATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGG  
CTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAAGACACAGACTTAACAATTTTAGATG  
GAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATTTCTTGAAGTTAATGGAACTT  
TTCTTTGGCTTTTCCAGTTGTGACCCGTTTTTCCAACCAAGTTCTGCAGCATATTAGATTCT  
AGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATATCACCAGTCATACACA  
GCCTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAAGTGCTCATTAGG  
TTTTATAACAAGAAGCTACATTTTTTGCCCTTAAGACACTACTTACAGTGTTATGACTTG  
TATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTTACATTTCCCTTC  
ACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCCTTC  
CCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAAACAGTAAATC  
CTAAATTCAAACCTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACATATGAGACAC  
ATCTTGTTTTACTGAATTTCTTCAATATTCCAGGTGATAGATTTTTTGTCG

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALT  
VTWNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGT  
YTCQVKNPPDVGIVIGEIRLSVVHTVRFSEIHFLALALIGSACALMIIVIVVVLQFQHYRK  
KRWAERAHKVVEIKSKEEERLNQEKVSVYLEDTD

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACC**ATGA**AGTTCTTAGCAGTCCTG  
GTACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCA  
GCTGACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACT  
GCTGCTGCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACC  
ACTGCTCGTAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGA  
GTGTGTCCCT**TGA**GATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTATGCT  
TCCTGTGATTTTCATCCAACTACTTACCTTGCTACGATATCCCCTTTATCTCTAATCAGT  
TTATTTTCTTTCAAATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPT  
 ATTAASTTARKDIPVLPKWVGDLPNGRVCP



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## FIGURE 190

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPPVIRMNGDK  
FRRLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVD  
FDEGSDVFQMLNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRV  
IRPPNYAGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIR  
GPPYAHKNPHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRK  
IMCVAGIGLVVLFSSWMLSIFRSKYHGYPSFLMS

**Signal peptide:**  
amino acids 1-29

**Transmembrane domains:**  
amino acids 183-205, 217-237, 217-287, 301-321

## FIGURE 191

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCA  
 AGAGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGC  
CATGGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGG  
 CACACTGGTTGCCATGCTGCTCCCCAGCTGGAAAAACAAGTTCTTATGTCCGTGCCAGCAT  
 TGTGACAGCAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGG  
 CATCACCCAGTGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGC  
 CCAGGCCATGATGGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGT  
 GGGCATGAGATGCACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGC  
 AGGTGGAGTCTTTTTTCATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCT  
 TCATGGGATCCTACGGGACTTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGAT  
 TGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCAT  
 CCTCTGCTTTTTCCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGC  
 CCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA  
 GTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGT  
 GGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACC  
 ACTGGATCGTGTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCA  
 AAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCA  
 TGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAA  
 CTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCT  
 GGGACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGA  
 CCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT  
 GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGG  
 CCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGCAT  
 GAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGA  
 GGACAGGAAGGCAGCCTGGGACATTTAAAAAATA



## FIGURE 193

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCA  
 TTTTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTT  
 ACCTGATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGC  
 ACTGTTGCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCA  
 CCTTCAGAGTCTGCTTTGAGCAGTGCTGCCCTTGGACCTTCATGGTGAAGCTGATAAACC  
 AGAACTGCGACTCAGCCCGGACCTCGGATGACAGGCTTTGTTCGAGTGTTCAGCTTAATGGA  
 ACATCAGGGGAACGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCT  
 GGTGTTACCTGAGATCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTC  
 AACTGCCCCACTTCATTCTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGC  
 CCACAGGTCCCCTTCTAGAATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAG  
 GGAATCTGAACCCTCCTGATGACCCCTATGGCCAACATCAACCCGGCACCAACCCCAAGGC  
 TGGCTGGGGAACCCTTCACCCTTCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATC  
 CAGGAGCAAAGCACAGGATCATAATAAATTTATGTACTTTATAAATGAAAA

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## FIGURE 194

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM LCQPHKRCGDKFYDPLQHCCYDDAV  
VPLARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**  
amino acids 1-24

## FIGURE 195

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATG  
ATGCTA CACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCC  
ATTGCAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGAC  
ATCACTTGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCA  
TTAATGGTTATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTT  
GCCCCAAATGAAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATG  
CATGAAACCACTGATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTT  
GTAGACCCTTCTTTAACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTAC  
ACATATGAGCCTCGGGATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAGACTT  
ATTCAGTCAGAGCTATAAGAGATGATGGAAAAAAGCCTTCACTTCAAAGAAGTCAAATTT  
CATGAAGAAAACCTCTGGCACATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTA  
ATATTACTATTTAGTTTTTTTTTAATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTT  
AAATCTGA

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## FIGURE 196

MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTL SRGWGDDITWVQTYEEGLFYAQKSKK  
PLMVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIM  
FVDPSLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation site:**

amino acids 51-57



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## FIGURE 197

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCCGAGCGCTCACTCGCTCGCACTC  
 AGTCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCCGCCGCTCCCCGGCACCAGAAAGTTC  
 CTCTGCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGC  
 TGGGGATCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTC  
 AAGGTCGCCACGCCGTATTCCCTGTATGTCTGTCCCAGAGGGGAGAACGTCACCCTCACC  
 TGCAGGCTCTTGGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTAC  
 CGCAGCTCGAGGGGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACG  
 TTCCAGGACCTTCACCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTG  
 GCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATG  
 CGAACCTGACCCTGCTGGATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCAC  
 CACCACTCGGAGCACAGGGTCCATGGTGGCATGGAGCTGCAGGTGCAGACAGGGCAAAGAT  
 GCACCATCCAACCTGTGTGGTGTACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCT  
 GCAGCCCTGGCTACGGGTGCCTGCATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTC  
 CTGGTCTACAAGCAAAGGCAGGCAGCCTCCAACCGCCGTGCCAGGAGCTGGTGGGATG  
 GACAGCAACATTCAAGGGATTGAAAACCCCGGCTTTGAAGCCTCACCACCTGCCAGGGG  
 ATACCCGAGGCCAAAGTCAGGCACCCCTGTCTATGTGGCCAGCGGCAGCCTTCTGAG  
 TCTGGGCGGCATCTGCTTTTCGGAGCCACGCCCTGTCTCCTCCAGGCCCGGAGAC  
 GTCTTCTTCCCATCCCTGGACCTGTCCCTGACTCTCCAACTTTGAGGTCATCTAGCCC  
 AGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGGGGCAGGTGCATTTGAGCCAGGGCT  
 GGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTCCCTCCCTCCTGCTCTGGGCTCA  
 GATACTGTGACATCCAGAGCCAGCCCTCAACCCCTCTGGATGCTACATGGGGATGC  
 TGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAGATTCTCCCTAGAGACCT  
 GAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAAGTCTCAGAACGTCCAG  
 CCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCAGCATCAGTGGGACA  
 AGATGGACACTGGGCCACCTCCCAGGCACCAGACACAGGGCACGGTGGAGAGACTTCTC  
 CCCCCTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTCTCAGACTTCCTC  
 TTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCCACCTTCCC  
 CAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAATCTGGGG  
 CTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTACATAT  
 TGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAGAT  
 GTTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCTACTCCCACTGCTCAGCGCGGG  
 CCATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCG  
 GGATGCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAGA

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## FIGURE 198

MGVPTALEAGSWRWGSLFLAASLGPVAAFQVATPYSLYVCPEGQNVTLTTCRLLGPV  
DKGHDVTFYKWTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLE  
SASDHGNGFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVV  
YPSSSQDSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRRAQELVRMDSNIQGI  
ENPGFEASPPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFVPSLD  
PVPDSPNFVI

**Signal peptide:**  
amino acids 1-28

**Transmembrane domain:**  
amino acids 190-216

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## FIGURE 199

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTC  
 CCGTGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCCTTGCGGAAAATGCTGATCT  
 CAGTCGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCC  
 CGGGAGAGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCA  
 GGGAGGAGGCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCA  
 CGCAGGAGAACGTGGCCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCGCCAGCG  
 GGAGGTCACCGTGAGACCGGACTTGCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGG  
 AATCCGAGGCAGCCTTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATG  
 CCAGGACTCTCCGGGGTCCTGTGAGCTGCCGTCGGGTGAGCACGTTTCCCCCAAACCTG  
 GACTGACTGCTTTAAGGTCCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTG  
 AACTGAAAGAACCAATAAAATCATGTTCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 200

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLL  
LATLQEAATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**  
amino acids 1-18

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCTCCGCTCACGC  
AGAGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAAT  
CCATCCGTCACCTCTCCTGTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACAT  
CC**ATGG**GCTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGC  
AGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCCTTGGTGGGGGAGGACGCAGCATTCTCCT  
GTTTCCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCCTCAGGGGGCCAGT  
TCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCAC  
AGTATCAAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGGCGCATCTCTCTGA  
GGCTGGAAAACATTACTGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCTCAGT  
CTTACTACCAGAAGGCCATCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCA  
TTTCCATCACGGGATATGTTGATAGAGACATCCAGCTACTCTGTCTCAGTCTCGGGCTGGT  
TCCCCCGGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCA  
GGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGA  
ACGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCA  
GGGTACAGATAGGAGATACTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTAC  
TGGGAATACTCTGCTGTGGCCTATTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCA  
AATTCAGTGGAAAATCCAGGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAAT  
TGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGA  
AGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTC  
ACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGA  
AACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGG  
ATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCC  
TCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGTTTTATCAGCGTCTTCC  
CCAGGACCCACCTACAAAAATAGGGGTCTTCTGACTATGAGTGTGGGACCATCTCCT  
TCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTGCGTTTGAAGGCTTAT  
TGAGGCCCTACATTGAGTATCCGTCTCTATAATGAGCAAAATGGAACCTCCATAGTCATCT  
GCCAGTCAACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCAG  
AGACAAGCAACAGTGAGTCCCTCTCACAGGCAACACGCCCTTCTCTCCCAGGGGTGAAA  
TG**TAGG**GATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCAGATC  
CAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCCAC  
ATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAAC  
CGTCAGGAATTCCCATCTCACAGGCTGTGGTGATGATTAAAGTAGACAAGGAATGTGAATA  
ATGCTTAGATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTTCATTATATTACACTT  
TCAGTAAAAAAA

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**FIGURE 202**

MALMLS LVL SLLKLGSGQWQVFGPDKPVQALVGEDAAFS CFLSPKTNAEAMEVRFRRGQF  
SSVVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCR ISSQS  
YYQKAIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFP RPPTAKWKGPQGQDLSTDSR  
TNRDMHGLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVL  
GILCCGLFFGI VGLKIFFSKFQWKIQAE LDWRRKHGQAE LRDARKHAVEVTLDPETAHPK  
LCVSDLKTVTHRKA PQEVP HSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRD  
DVD RRKEYVTLS PDHGYWVLR LNGEHL YFTLNPRFISVFPRT PPTKIGVFLDYECGTISF  
FNINDQSLIYTLT CRFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPE  
TSNSESSSQATT PFLPRGEM

Signal peptide:  
amino acids 1-17

Transmembrane domain:  
amino acids 239-255

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## FIGURE 203

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTT  
 GGTCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCT  
 TGGGCCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGA  
 CATGAAGAACGTCGTGGGGGTGGTGGTGACCCCTCACTCCAGAAAACAACCTGCGGACGCT  
 GTCCTCTCAGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAA  
 CTCCGGATGGGTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCAC  
 CAACTTCAGAGACTATGCCATCATCTTCACTCAGCTGGAGTTTCGGGGACGAGCCCTTCAA  
 CACCGTGGAGCTGTACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCAC  
 CAAGTGGAGCAGGAGCCTGGGCTTCCTGTGACAGTAGCAGGCCCAGCTGCAGAAGGACCT  
 CACCTGTGCTCACAAGATCCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCCACA  
 GGGTCCTGTGACCTCGGCCAGTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGGCCCAGCA  
 CCAGCTCAGAATAAAGCGATTCCACAGCA

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## FIGURE 204

MGGLLLAAFLALVSVPRQA VVLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVV  
VTILTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAI I  
FTQLEFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**  
amino acids 1-20



GACCCCCAGTGACCTGCCGAGGTCGGCAGACAGAGCTCTGGAGATGAAGACCCTGTTCC  
TGGGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGAGGAGGATATCA  
CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGC  
CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT  
TCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGG  
AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCCA  
GGAGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCCTGCTCCACATGG  
GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAAT  
TGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTTCACGCCCTGCAGACGGGAAGCT  
GCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAG  
ACACAGAGCCCGGACCACTTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCC  
ACCTGACTCCAAATAAAGTCCTTTTCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

amino acids 1-17

GTTCCGCGAGATGCAGAGGTTGAGGTTGGCTGCGGGGACTGGAAGTCATCGGGCAGAGGTCTC  
 ACAGCAGCCAAGGAACCTGGGGGCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAG  
 TTAATCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGG  
 TTCGAGTGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTA  
 CTCTGTGGGGCGACGCTCATCGCCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAG  
 CCCCCTACATAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAG  
 ACCCGGACAGCCACTGAGTCCTTCCCCCACCCTGGCTTCAACAACAGCCTCCCCAACAAA  
 GACCACCGCAATGACATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCT  
 GTGCGACCCCTCACCTCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCC  
 GGCTGGGGCAGCACGTCCAGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAAC  
 ATCACCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACC  
 ATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGC  
 CCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCG  
 ATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAATATGTGGACTGGATCCAGGAG  
 ACGATGAAGAACAAATTAGACTGGACCCACCCACCACAGCCCATCACCTCCATTTCCACT  
 TGGTGTTTGGTTCCCTGTTCACTCTGTTAATAAGAAACCCTAAGCCAAGACCCCTCTACGAA  
 CATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATCAACCTGGGGTTTC  
 GAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATGTGACTCTGGGAATGACA  
 ACACCTGGTTTGTCTCTGTGTATCCCCAGCCCCAACAGCAGCTCCTGGCCATATATCA  
 AGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAA

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## FIGURE 208

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTA  
AHCLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV  
SITWAVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRCANITIIHQKCENAYPG  
NITDTMVCASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYV  
DWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site:**

amino acids 58-63

**N-glycosylation sites:**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site:**

amino acids 145-148

**Kringle domain proteins:**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein:**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins:**

amino acids 222-249, 189-222

# FIGURE 209

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTC  
GCCGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTC  
AGCAACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGG  
CTGGCCGAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTT  
CCAGAAAAGCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGC  
GAGATTGACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCAC  
CTGGAGATGAAGAAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTAC  
CGAGACTTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATG  
TTTGAAGGAAAAGCCAACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGAC  
ATTGCTAGCCTGCCCTGAGGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCC  
CTCCCGATCTTGCTGCCCTTCTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGT  
CATTGAGGGTTTGTGTTTGTGTTTTCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTA  
AAGGGGCTCTGGGTGCGGGAATCCTGAGCCTTGGGTCCCCCTCCCTCTCTTCTTCCCTCCT  
TCCCCGCTCCCTGTGCAGAAGGGCTGATATCAAACCAAAAACCTAGAGGGGGCAGGGCCAG  
GGCAGGGAGGCTTCCAGCCTGTGTTCCCCCTCACTTGAGGAACCAAGCACTCTCCATCCTT  
TCAGAAAGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCCAAGC  
CACTCTGAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTCCCTTGG  
ACAGTGCCATGGTTCCAGTGCTCTGGTGTCAACCAAGGACACAGCCACTCGGGGCCCCGCT  
GCCCCAGCTGATCCCCACTCATTCCACACCTCTTCTCATCCTCAGTGATGTGAAGGTGGG  
AAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGGTACCAGAAGGAACCTTCCAGTC  
CTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAGCGTGACGCCCTACTGTCCCT  
TACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTGGGGTTTGGGGGGAAAGGT  
CAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGACCAGGATGGGAGAATGA  
GGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGACTGAGAAATACAAG  
GTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 210

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEFD  
LNNEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVL  
KLVMMFEGKANESSPKPVGPPPERDIASLP

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATG  
AGGAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTC  
CCAGCACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCA  
GAGAAGGCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTG  
CTGTTCCCTGTCCAGAAGCCGAAACTCTTTGACCACCGAGGAGAAGCCACGAGGTTCAGGGC  
AGGGGCCCCATCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGT  
GTCTTGAGTCCCGAGCCCCGACCATGACAGCCTGTATCACCCTCCGCCTGAGGAGGACCAG  
GGCGAGGAGAGGCCCCGTTGTGGGTGATGCCAAATCACCAGGTGCTCTGGGACCGGAG  
GAAGACCAAGAGCCACATCTACCAACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGC  
CCTGTCCCAAGGCCCAGGCTGTTGGGACTGGGACCCTCCCTACCTTGCCCCAGCTAGACA  
AATAAACCCCAGCAGGCACAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 212

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLV  
VLFPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEED  
QGEERPRLWVMPNHQVLLGPPEEDQDHIYHPQ



## FIGURE 213

CAGGCAGAAGCGAACAAAGACCCAGCAAGAGAAGGCAGAGGCTAAGACCCATCCCGTATC  
TGCTCTCCTGAAATAATTCTGGAGTCAATGCCTGAAATGCCAGAGGACATGGAGCAGGAGG  
AAGTTAACATCCCTAATAGGAGGGTTCTGGTTACTGGTGCCACTGGGCTTCTTGGCAGAG  
CTGTACACAAAGAATTTTCAGCAGAATAATTGGCATGCAGTTGGCTGTGGTTTCAGAAGAG  
CAAGACCAAAATTTGAACAGGTTAATCTGTTGGATTCTAATGCAGTTCATCACATCATTC  
ATGATTTTTCAGCCCCATGTTATAGTACATTGTGCAGCAGAGAGAAGACCAGATGTTGTAG  
AAAATCAGCCAGATGCTGCCTCTCAACTTAATGTGGATGCTTCTGGGAATTTAGCAAAGG  
AAGCAGCTGCTGTTGGAGCATTTCTCATCTACATTAGCTCAGATTATGTATTTGATGGAA  
CAAATCCACCTTACAGAGAGGAAGACATAACCAGCTCCCCTAAATTTGTATGGCAAAACAA  
AATTAGATGGAGAAAAGGCTGTCTGGAGAACAATCTAGGAGCTGCTGTTTTGAGGATTC  
CTATTTCTGTATGGGGAAGTTGAAAAGCTCGAAGAAAGTGCTGTGACTGTTATGTTTGATA  
AAGTGCAGTTCAGCAACAAGTCAGCAAACATGGATCACTGGCAGCAGAGGTTCCCCACAC  
ATGTCAAAGATGTGGCCACTGTGTGCCGGCAGCTAGCAGAGAAGAGAATGCTGGATCCAT  
CAATTAAGGGAACCTTTCACTGGTCTGGCAATGAACAGATGACTAAGTATGAAATGGCAT  
GTGCAATTGCAGATGCCTTCAACCTCCCCAGCAGTCACTTAAGACCTAATTACTGACGCC  
CTGTCCTAGGAGCACAAACGTCCGAGAAATGCTCAGCTTGACTGCTCCAAATGGAGACCT  
TGGGCATTGGCCAACGAACACCATTTTCGAATTGGAATCAAAGAATCACTTTGGCCTTTCC  
TCATTGACAAGAGATGGAGACAAACGGTCTTTTCATTAGTTTATTTGTGTTGGGTTCTTTT  
TTTTTTTTAAATGAAAAGTATAGTATGTGGCACTTTTTTAAAGAACAAAGGAAATAGTTTTG  
TATGAGTACTTTAATTGTGACTCTTAGGATCTTTCAGGTAAATGATGCTCTTGCACTAGT  
GAAATTGTCTAAAGAACTAAAGGGCAGTCATGCCCTGTTTGCAAGTAATTTTTCTTTTTTA  
TCATTTTGTGTTGCTGGCTAAACTTGGAGTTTGAGTATAGTAAATTATGATCCTTAAAT  
ATTTGAGAGTCAGGATGAAGCAGATCTGCTGTAGACTTTTCAGATGAAATTGTTTATTCT  
CGTAACCTCCATATTTTTCAGGATTTTTGAAGCTGTTGACCTTTTCATGTTGATTATTTTA  
AATTGTGTGAAATAGTATAAAAATCATTGGTGTTCATTATTTGCTTTGCCTGAGCTCAGA  
TCAAAATGTTTGAAGAAAGGAACCTTATTTTTTGCAAGTTACGTACAGTTTTTATGCTTGA  
GATATTTCAACATGTTATGTATATTGGAACCTTCTACAGCTTGATGCCTCCTGCTTTTATA  
GCAGTTTATGGGGAGCACTTGAAAGAGCGTGTGTACATGTATTTTTTTTCTAGGCCAAACA  
TTGAATGCAAACGTGTATTTTTTTTAAATATAAATATATAACTGTCCTTTTCATCCCATGTT  
GCCGCTAAGTGATATTTTCATATGTGTGGTTATACTCATAATAATGGGCCTTGTAAGTCTT  
TTCACCATTTCATGAATAATAATAAATATGTACTGCTGGCATGTAATGCTTAGTTTTCTTG  
TATTTACTTCTTTTTTTTAAATGTAAGGACCAAACCTTCTAACTAATTGTTCTTTTGTGTC  
TTTAATTTTTTAAAAATTACATTCTTCTGATGTAACATGTGATACATACAAAAGAATATAG  
TTTAATATGTATTGAAATAAAAACACAATAAAATT

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## FIGURE 214

MPEMPEDMEQEEVNI PNRRVLVTGATG LLGRAVHKEFQQNNWHAVGCGFRRARPKEQVN  
LLDSNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAA SQLNVDA SGNLAKEAAAVGAFL  
IYISSDYVFDGTNPPYREEDI PAPLNLYGKTKLDGEKAVLENNLGAAVLRIPILYGEVEK  
LEESAVTVMFDKVQFSNKSANMDHWQQRFP THVKDVATVCRQLAEKRMLDPSIKGTFHWS  
GNEQMTKYEMACAIADAFNL PSSHLPITDSPVLGAQRPRNAQLDCSKLET LGIGQRTPF  
RIGIKESLWPFLIDKRWRQTVFH

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 105-127

**N-glycosylation site:**

amino acids 197-201

**N-myristoylation site:**

amino acids 303-309

**Short-chain dehydrogenases/reductases family proteins:**

amino acids 18-30

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## FIGURE 215

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCC  
CAGGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTT  
AAAGGACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCA  
CAGAATTGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGCACCTA  
GCCGCTAGCATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACC  
AGCGCCAGCCGGCTGCGGCTGCCCCACAGGCTCACCATGGGCTCCGGGCGCCGGGCGCTG  
TCCGCGGTGCCGGCCGTGCTGCTGGTCCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAG  
AACGACACGGAGCCCATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCG  
GCCACGGACTCCAAGGGCTCCTCTTCCCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAAC  
TCCAAGGTCGCCTTCTCGGCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAAC  
AAGACGCGCATCATTTACTTTCGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTG  
GAGTCTGTCTTTGTAGCACCAAGAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAA  
GTCTACCAGAGCCAACTATCCAGGTAACTTGTAGTTAAATGGAAAACAGTAATATCT  
GCCTTTGCGGGGGACAAAGATGTTACTCGTGAAGCTGCCACGAATGGTGTCTCTCTAC  
CTAGATAAAGAGGATAAGGTTTACCTAAACTGGAGAAAGGTAATTTGGTTGGAGGCTGG  
CAGTATTCCACGTTTTCTGGCTTTCTGGTGTTCCCCCTATTAGGATTCAATTTCTCCATGA  
TGTTCAATCCAGGTGAGGGATGACCCACTCCTGAGTTATTGGAAGATCATTTTTTTCATCAT  
TGGATTGATGTCTTTTATTGGTTTCTCATGGGTGGATATGGATTCTAAGGATTCTAGCCT  
GTCTGAACCAATAACAAATTTACAGATTATTTGTGTGTGTCTGTTTCAGTATATTTGGA  
TTGGGACTCTAAGCAGATAAATACCTATGCTTAAATGTAACAGTCAAAAGCTGTCTGCAAG  
ACTTATTCTGAATTTTCATTTCTGGGATTACTGAATTAGTTACAGATGTGGAATTTTTATT  
TGTTTAGTTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGAAAACCTCTAAAGTTCTGAC  
TTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTGTGTTAATATATTGATT  
ATATTTGTTTTTATTCTTTGGAATTAGTTTGTGTTGGTTCTTGTAACAAAACCTGGATTTT  
TTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAATGGCTTGCCAC  
AAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAAAGAATGCTTCA  
TAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATTTTCTAAGA  
AGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAGTGCTCA  
ATCCCTGAGCCTCAGCAAAACAGCTCCCCCTCCGAGGGAAATCTTATACTTTATTGCTCAA  
CTTTAATTAAAATGATTGATAATAACCACTTTATTAACCACTAAGGTTTTTTTTTTTTTC  
CGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACCTTTAAATTG  
TATATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCA  
ATATCTTGCTTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAA  
TAAAGATTAATATATGTTAAAAAAA

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## FIGURE 216

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPL  
GISVRAANSKVAFAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVVFVAPRKGIIY  
SFSFHVIVKQYQSQTIVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLE  
KGNLVGGWQYSTFSGFLVFPL

**Signal peptide:**  
amino acids 1-27

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## FIGURE 217

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTCGCTC  
TGGGCTTGCCCTTCTTGGTGCTCTTGGTGCCCTCGGTTCGAGAGCCATCTGGGGGTTCCTGG  
GGCCCAAGAACGTCTCGCAGAAAGACGCCGAGTTTGAGCGCACCTACGTGGACGAGGTCA  
ACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCCGCAACAGGACAGAGG  
GCGTGCGTGTGTCTGTGAACGTCCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG  
TCCGCCAGAAGGAGGCTGTGGTGTCCTTCCAGGTGCCCCCTAATCCTGCGAGGGATGTTTC  
AGCGCAAGTACCTCTACCAAAAAGTGGAACGAACCCTGTGTGACCCCCCACCAGAATG  
AGTCGGAGATTCACTTCTTCTACGTGGATGTGTCCACCCTGTCAACAGTCAACACCACAT  
ACCAGCTCCGGGTGACCCGCATGGACGATTTTGTGCTCAGGACTGGGGAGCAGTTTCAGCT  
TCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT  
CGGTAATTGTCAAGGTGACCTCCAACAAGGCCTTCCCCTGCTCAGTCATCTCCATTCAAG  
ATGTGCTGTGTCTGTCTATGACCTGGACAACAACGTAGCCTTCATCGGCATGTACCAGA  
CGATGACCAAGAAGGCGGCCATCACCGTACAGCGCAAAGACTTCCCCAGCAACAGCTTTT  
ATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCTCCCTGCCTTTCTACC  
CCTTCGCAGAAGATGAACCGGTGATCAAGGGCACCGCCAGAAAACCTGTGAGTGCTGG  
TGTCTCAAGCAGTCACGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGCCTGGGTATAT  
TTCTCTCCTTTTACCTGCTGACCGTCCCTCCTGGCCTGCTGGGAGAAGTGGAGCAGAAGA  
AGAAGACCCTGCTGGTGGCCATTGACCGAGCCTGCCAGAAAGCGGTACCCCTCGAGTCC  
TGGCTGATTCTTTTCCCTGGCAGTTCCCTTATGAGGGTTACAACATATGGCTCCTTTGAGA  
ATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG  
GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCT  
CTGTGGAGGAGGATGACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCAATC  
GCACCAAGCAATACCTCTATGTGGCTGACCTGGCACGGAAGGACAAGCGTGTTCTGCGGA  
AAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGCTGTCTTCTATGCCCTTCCTG  
TGGTGCAGCTGGTGATCACCTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT  
GCTACTACAACCTCCTCTGCGCCACCCACTGGGCAATCTCAGCGCCTTCAACAACATCC  
TCAGCAACCTGGGGTACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCCTGCAACGGG  
AGATCAACCACAACCGGGCCCTGCTGCGCAATGACCTCTGTGCCCTGGAATGTGGGATCC  
CCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGATGGAGGGGCTGCTCA  
GTGCTTGCTATCATGTGTGCCCAACTATAACCAATTTCCAGTTTGACACATCGTTTATGT  
ACATGATCGCCGGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACG  
CCAGCGCCTACAGTGCCTACGCCTGCCTGGCCATTGTGATCTTCTTCTCTGTGCTGGGCG  
TGGTCTTTGGCAAAGGGAACACGGCGTTCTGGATCGTCTTCTCCATCATTCACATCATCG  
CCACCCTGCTCCTCAGCACGCAGCTCTATTACATGGGCCGGTGGAACTGGACTCGGGGA  
TCTTCCGCCGCATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC  
TCTACGTGGACCGCATGGTGCTGCTGGTTCATGGGCAACGTGATCAACTGGTTCGCTGGCTG  
CCTATGGGCTTATCATGCGCCCCAATGATTTGCTTCCCTACTTGTGGCCATTGGCATCT  
GCAACCTGCTCCTTTACTTCGCCTTCTACATCATCATGAAGCTCCGGAGTGGGGAGAGGA  
TCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCTGGGGCTTCGCGCTCT  
TCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCGAGGGAGCACA  
ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCCTCTCCT  
CCATCGCCATGTTCCGGTCCCTCCTGGTGTGCTGACACTGGATGACGACCTGGATACTG  
TGCAGCGGGACAAGATCTATGTCTTCTAGCAGGAGCTGGGCCCTTCGCTTCACCTCAAGG  
GGCCCTGAGCTCCTTTGTGTGATAGACCGGTCACTCTGTGCTGCTGTGGGGATGAGTCCC  
AGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT  
GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCGAGGAGCAGGCCTGC  
TCCCCTGGAACCCCCAGATGTTGGCCAAATTGCTGCTTCTTCTCAGTGTTGGGGCCTTC

CATGGGCCCCCTGTCCTTTGGCTCTCCATTTGTCCCTTTGCAAGAGGAAGGATGGAAGGGA  
 CACCCTCCCCATTTTCATGCCCTTGCAATTTTGCCCGTCCTCCTCCCCACAATGCCCCAGCCT  
 GGGACCTAAGGCCTCTTTTTTCTCCATACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA  
 ATCTCTGTCCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGC  
 CCATTCCAGTCAGCCAGGATGGATGGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGC  
 CAGACTTTTGGTGCTAAGGCCTGCAAGGGGCCTGGGGCAGTGCGTATTCTCTTCCCTCTG  
 ACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATTTGAGAACCGCCTTCT  
 GATTCAAGAGGCTGAATTCAGAGGTCACCTCTTCATCCCATCAGCTCCCAGACTGATGCC  
 AGCACCAGGACTGGAGGGAGAAGCGCCTCACCCCTTCCCTTCTTTCCAGGCCCTTA  
 GTCTTGCCAAACCCCAGCTGGTGGCCTTTTCAGTGCCATTGACACTGCCCAAGAATGTCCA  
 GGGGCAAAGGAGGGATGATACAGAGTTTCAGCCCCTTCTGCCTCCACAGCTGTGGGCACCC  
 CAGTGCCCTACCTTAGAAAGGGGCTTCAGGAAGGGATGTGCTGTTTCCCTCTACGTGCCCA  
 GTCCTAGCCTCGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCAGGCA  
 AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGC  
 CCCAGCTCTGGGCACCCTGGCCACCCTGGTCCTTGGATCCCCTTCGTCCCACCTGGTCCA  
 CCCCAGATGCTGAGGATGGGGGAGCTCAGGCGGGGCCTCTGCTTTGGGGATGGGAATGTG  
 TTTTCTCCCAAACCTTGTTTTTATAGCTCTGCTTGAAGGGCTGGGAGATGAGGTGGGTCT  
 GGATCTTTTCTCAGAGCGTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATT  
 TGCATTCAATAAACAACCAGACTCAAAAAAAAAAAAAAA

## FIGURE 218

MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRN  
 RTEGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPP  
 TKNESEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRRTGEQFSFNTTAAQPQYFKYEFPE  
 GVDSVIVKVTSNKAFFPCSVISIQDVLCVPYDLNNAFIGMYQTMTKKAAITVQRKDFPS  
 NSFYVVVVVKTEDQACGGSPLFYPPFAEDEPVDQGHRQKTL SVLVLSQAVTSEAYVSGMLFC  
 LGIFLSFYLLTVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNYG  
 SFENVSGSTDGLVDSAGTGDL SYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDK  
 NVIRTKQYLYVADLARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVNVTGN  
 QDICYYNFLCAHPLGNLSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALE  
 CGIPKHFGLFYAMGTALMMEGLLSACYHVCPNYTNFQFDTSFMYMIAGLCMLKLYQKRHP  
 DINASAYSAYACLAIVIFFSVLG VVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKL  
 DSGIFRRILHVLYTDCIRQCSGPLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLA  
 IGICNLLLYFAFYIIMKLRSGERIKLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAES  
 REHNRDCILLDFDDHDIWHFLSSIAMFGSFLVLLTLDDDLDTVQRDKIYVF

### Important features of the protein:

#### Signal peptide:

amino acids 1-18

#### Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

#### Leucine zipper pattern:

amino acids 497-518

#### N-glycosylation sites:

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168,  
 364-367, 476-479, 496-499, 572-575, 603-606, 699-702





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## FIGURE 220

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQML  
TLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTTILSSEELP  
QIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLPTPSGTDD  
DFAVTTTLAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**  
amino acids 1-16

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Amino acids 16-22;224-230;464-470;637-643;698-704

[illegible]

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## FIGURE 224

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLV  
LETPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHS  
LTVPSKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVK  
KKTQGKVVDIIQGLDLLTAMVLVNHIFFKAKWEKPPFHLEYTRKNFPFLVGEQVTVQVPMM  
HQKEQFAFGVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQK  
RWIEVFIPRFSISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVS  
EEGTEATAATTTKFIVRSKDGPSYFTVSNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**  
amino acids 1-20

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## FIGURE 225

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCT  
TCCCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGG  
GGCCCTGTCTGGATGGGCGGCCAGCGATGACCCCATTTGAGAAGGTCATTGAAGGGATCAA  
CCGAGGGGCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGG  
AATCACGCATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAG  
CCACACCGGCAAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGT  
TGCCCATGAGATCAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCA  
TGGGGTCAACAACGCTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTT  
CCACACTGGGGTCCACCAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCA  
TGCTGCTGACCAGGCTGGAAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGC  
TGGCCAGGCCGGGAAGGAGCTGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGA  
GGCCAACCAGCTGCTGAATGGCAACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGC  
CACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGC  
CCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGGCATCCGGCCTTGCTGGGAGAA  
TAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGGTTGGGGGTGGGGGACAGG  
TTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTGTGAATAAACTTGATACACCA

amino acids 35-225

## FIGURE 227

GAAGTAGAGGTGTTGTGCTGAGCGGCGCTCGGCGAACTGTGTGGACCGTCTGCTGGGACT  
 CCGGCCCTGCGTCCGCTCAGCCCCGTGGCCCCGCGCACCTACTGCC**AT**GGAGACGCGGCC  
 TCGTCTCGGGGCCACCTGTTTGCTGGGCTTCAGTTTCCTGCTCCTCGTCATCTCTTCTGA  
 TGGACATAATGGGCTTGGAAGGGTTTTGGAGATCATATTCAATTGGAGGACACTGGAAGA  
 TGGGAAGAAAGAAGCAGCTGCCAGTGGACTGCCCCCTGATGGTGATTATTCATAAATCCTG  
 GTGTGGAGCTTGCAAAGCTCTAAAGCCCCAAATTTGCAGAATCTACGGAAATTTCAGAACT  
 CTCCCATAATTTTGTTATGGTAAATCTTGAGGATGAAGAGGAACCCAAAGATGAAGATTT  
 CAGCCCTGACGGGGGTATATTTCCACGAATCCTTTTTCTGGATCCCAGTGGCAAGGTGCA  
 TCCTGAAATCATCAATGAGAATGGAAACCCAGCTACAAGTATTTTTATGTCAGTGCCGA  
 GCAAGTTGTTCAAGGGATGAAGGAAGCTCAGGAAAGGCTGACGGGTGATGCCTTCAGAAA  
 GAAACATCTTGAAGATGAATTG**TAA**CATGAATGTGCCCCCTTCTTTCATCAGAGTTAGTGT  
 TCTGGAAGGAAAGCAGCAGGGAAGGGAATATTGAGGAATCATCTAGAACAATTAAGCCGA  
 CCAGGAAACCTCATTCCTACCTACACTGGAAGGAGCGCTCTCACTGTGGAAGAGTTCTGC  
 TAACAGAAGCTGGTCTGCATGTTTGTGGATCCAGCGGAGAGTGGCAGACTTTCTTCTCCT  
 TTCCCTCTCACCTAAATGTCAACTTGTCAATTGAATGTAAAGAATGAAACCTTCTGACAC  
 AAAA



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## FIGURE 228

METRPRLGATCLLGFSFLLLVISSDGHNGLGKGFGDHIHWRTLEDGKKEAAASGLPLMVI  
IHKSWGACKALKPKFAESTEISELSHNFVMVNLEDEEEKDEDFSPDGGYIPRILFLDP  
SGKVHPEIINENGNP SYKYFYVSAEQVVQGMKEA QERLTGDAFRKKHLEDEL

**Signal peptide:**  
Amino acids 1-23

**Thioredoxin family proteins Homology Block:**  
Amino acids 58-75

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## FIGURE 229

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGGCTTCT  
 CTTTTCCCTCCGACGCGCCACGGCTGCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTC  
 CCCGAACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTG  
 GTCTCGGAGAAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGA  
 CGCGAGTTGGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACG  
 CCCTAGCCCGGTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCC  
 GCCCCACGCGGGTGC CGCGCCGCGCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGC  
 CGCTGCTACCCCTGCGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGA  
 CGGCGGCTCCCGGTGGCGGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGC  
 CGCGCTCCCCGCCCCGCCCCGCCCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGAT  
 GGCAGTTGGCGCGCTCTCCAGTTCCTTCTGCTCACCTGCTGCCTGATGGTGGCTCTGTG  
 CAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAA  
 GCGTGAGCACGCCACTCGGGACGGCCCCGGGGCGGGTGAACGAGCTCGGGCGCCCCGGCGAG  
 GGACGAGGGCGGCAGCGGCCGGGACTGGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCG  
 TGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGG  
 GGATCTGCAGGTCCGGCCCCGCGGGGACACCCCGCAGGCGGAAGCCCTGGCCGCAGCCGC  
 CCAGGACGCGATTGGCCCCGGAACCTCGCGCCACGCCCGAGCCACCCGAGGAGTACGTGTA  
 CCCGGACTACCGTGGCAAGGGCTGCGTGAGACGAGAGCGGCTTCGTGTACGCGATCGGGGA  
 GAAGTTCGCGCCGGGGCCCCCTCGGCCCTGCCCGTGCCTGTGCACCGAGGAGGGGCCGCTGTG  
 CGCGCAGCCCCGAGTGCCCGAGGCTGCACCCGCGCTGCATCCACGTGACACGAGCCAGTG  
 CTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCCGGGGCAAGACCTATCAGAC  
 TTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTGTGAAGCCAACGGTGAGGT  
 GCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACCCTGTGTACGAGCCTGA  
 TCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAAACCGCGGTGATCCC  
 TGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGG  
 CACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGAC  
 GCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAACATTCTAG  
 ATGACTCTGGGAACATATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTGTTG  
 GTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTCAAAA  
 CATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAGTA  
 AGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG  
 CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAA  
 AAAAAAAAAAAAAAAAAAAAAA

## FIGURE 230

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVN  
ELGRPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQA  
EALAAAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKEKFAPGPSACPCLC  
TEEGPLCAQPECPR LHPRCIHVDT SQCCPQCKERNYCEFRGKTYQTLEEFVVSPCERCR  
CEANGEVLCTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTIC  
HCTYEEGTWRIERQAMCTRHECRQM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site:**

amino acids 80-83

**N-myristoylation sites:**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence:**

amino acids 114-117

**EGF-like domain cysteine pattern signature:**

amino acids 176-187

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## FIGURE 232

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSI  
FMLSPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVII  
MNHRTMRMDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKS  
HFEDMIDYFCDIHEPLQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGFTF  
VVDRLREGKNLDAVHDITVAYPHNIPQSEKHLLQGDFPREIHFHVHRYPIDTLPTSKE  
DLQLWCHKRWEEKEERLRSFYQGEKNFYFTGQSVIPPCKSELRLVLVVKLLSILYWT  
LFSPLAMCLLIYLYSLVKWYFIITIVIFVLQERIFGGLEIIEELACYRLLHKQPHLNSK  
KNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

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## FIGURE 233

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATC  
TTGGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTG  
TTACTGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTC  
CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATA  
TTCAAGATAGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATAC  
TATTACTCCAATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGG  
GACATCTTATGCAATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA  
ACCTATATCTGTGAAATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA  
CTGCATGTGCTTCCAGAGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAG  
ATGGGATGTGTTTTCCAGAGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTT  
TCAGGACGGCGCGCAAAGGAGGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCT  
GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATT  
TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTAC  
ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGC  
CCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGT  
AATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTGCTGCTCCCTGTTCTG  
ATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCAGTGAATTCTACAGTCTTGGTG  
AAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCTGCCATTTTGAAAGATGT  
GAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAAGAAGAA  
CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTGAGG  
TCAGATCGGAACAACTCACTTGAAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA  
GCCTTTTTGAGAAGAATGGAGAGTCCCTTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTG  
TGTGTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTCCCAGCTGTCTCCTGT  
CTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGAC  
AGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGG  
ACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGATCAGACC  
CTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAAACCAA  
CCCAAATCAA

## FIGURE 234

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS  
PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTIYICEIRL  
KGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE  
IVFRYYHKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGN  
LVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLPVLLILIVKKTC  
GNKSSVNSTVLVKNTKKTNPETKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEAT  
YMTMHPVWPSLRSDRNNLEKKS GGGMPKTQQAF

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## FIGURE 235

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGA  
GAAAGAACTGACTGAAACGTTTGGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTT  
GGCAGTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAG  
TGACAGCGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTTCGCCC  
ACTTCCACCAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAAT  
ACCTGAATCTGCCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCA  
CGATAAACCTGGTCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCT  
GTTAATAAAAGAAAAACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCT  
TTAGTGATCTTCTTTAATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA



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## FIGURE 236

MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPR  
FPWFRRNFPIPIPIESAPTTPLPSEK

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

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## FIGURE 237

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGG  
TGAATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTTCATCGGCAACA  
GCATCGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCA  
CCGGCCAGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGG  
CTGCACGTGCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACC  
TTGCTGGGGCCAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGC  
TCACCTCTGGGATTGTCTTTGTTCATCTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGA  
CGGCGCATGCCATCATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGG  
AGCTGGGGGGCCTCCCTCTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGCTGGGTGGG  
GGTTGCTGTGCTGCACTTGCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCC  
GCTACTCAACATCTGCCCCCTGCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATT  
ACGTCTTGACGTGGAGGGGAATGGGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAG  
TGCCCAACAGCTTTGGGATGGGTTTCGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTT  
TGACTGAGGATATTTAAAATTCATTTGAAAACCTGAGCCAAGGTGTTGACTCAGACTCTCA  
CTTAGGCTCTGCTGTTTCTCACCCCTTGATGATGGAGCCAAAGAGGGGATGCTTTGAGAT  
TCTGGATCTTGACATGCCCATCTTAGAAGCCAGTCAAGCTATGGAACATAATGCGGAGGCT  
GCTTGCTGTGCTGGCTTTGCAACAAGACAGACTGTCCCCAAGAGTTCTGCTGCTGCTGG  
GGGCTGGGCTTCCCTAGATGTCACTGGACAGCTGCCCCCATCCTACTCAGGTCTCTGGA  
GTCCTCTCTTCACCCCTGGAAAAACAAATCATCTGTTAACAAAGGACTGCCACCTCCG  
GAATTCTGACCTCTGTTTCCCTCCGTCTGATAAGACGTCCACCCCCCAGGGCCAGGTCC  
CAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACCCTTCTGCCCTGCCCCCTCG  
TCTACCCCCCTTTACACTCACATTTTTATCAAATAAAGCATGTTTTGTAGTGCA

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## FIGURE 238

MASAGMQILGVVLTL LGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEG LWMSCVVQSTG  
QMCKVYDSL LALPQDLQAARALCVIAL LVALFGLLVYLAGAKCTTCVEEKDSKARLVLT  
SGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKREL GASLYLGWAASG LLLLLGGGL  
LCCTCPSGGSQG PSHYMARYSTSAP AISRGPSEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGG  
GTCTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGT  
CTCCAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCC  
CCATCACATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCCT  
TGTGTACCGAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCT  
AAATTCTCCATGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCC  
AGGCTCTGACTGAGTTTCTTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGAT  
TCAGAGTAATCTTGACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTC  
ACTGACAGACCAGCATTTTTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA

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## FIGURE 240

MKITGGLLLLCTVVYFCSSEEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITY  
GNECHLCTESLKSNGRVQFLHDGSC

**Signal peptide:**  
amino acids 1-19

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## FIGURE 241

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGC  
CCCGCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCG  
CTGCTCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATG  
CTTCAAAAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAA  
GCCAAAGAATTCTTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGG  
CCCGAGGTGCAGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTT  
GAAGATGACATCACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGAT  
TACTACCAACGTCACCTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTT  
AGGCATGGAGCCAGCGTCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACA  
AGAAGCAAATAGCGATTCTCTTCATGTATCTCCTAATGCCTTACACTACTTGGTCTCTGA  
TTTGCTCTATTTTCAGCAGATCTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAA  
AACAACACATGTAAATGCCTTTTGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAA  
ATAAAGCATTTTGTTAAAAAGA

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## FIGURE 242

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKLMLQKREAPVPTKTKVAVDENKAKE  
FLGSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYDYYQ  
RHYDEDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**  
amino acids 1-30

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## FIGURE 243

CTCCATTAAACCACCACCAGCTCCCCAAGCCACCCCTTCAGCCATGAAGTTCCTGCTCCT  
GGTCTTGGCAGCCCTCGGATTCTTGACCCAGGTGATCCCAGCCAGTGCAGGTGGGTCAAA  
ATGTGTGAGTAACACCCCAAGGATACTGCAGGACATGTTGCCACTGGGGGGAGACAGCATT  
GTTTCATGTGCAACGCTTCCAGAAAATGCTGCATCAGCTACTCCTTCCCTGCCGAAGCCTGA  
CCTACCACAGCTCATCGGTAACCACTGGCAATCAAGGAGAAGAAACACACAAAGGAAAGA  
CAAGAAGCAACAAACGACCGTAACATCATTAATATAACCACTGCTATCGCCTCCACCAACTCA  
GAGAAATATCATTTCCACAGTTCCAATTCCTCCTACATTGCTGAGTACTAGCCAAGGCTC  
CTCTTTATGGGGCAGATATCTATAGCCAACCCCAAACTTCTGTCTTCTATCATTCTGTCT  
ATTTCATCTAGTAACATAATTTGGAGTTTGTATCTATCTTACGAGAACAAATCATCATGCAGA  
TTCGTCCACAGGGGATCTGTGAGTTTGGGTCTTCCAAATGAAAAATGTCAAGACAGAATT  
GGACATGCAAAAGATTGACTGGGAGAACACACCTCTGATGGACAAAGGTGAGACAGAGCA  
GCCACAGGCAGGGAGAGCCTTCAGACTGCAACGCTGGCCTGATACGTGTCAAAGGAGAGA  
GGGATAGAGGAGGATTGAATAGAAGGAGACTAAGACTGCAGCTCTAAGAAAGTCTCAGCC  
AAACAGATGGGGAGGCCCAAAGCAAGGCTTGCCCTCAGAGGAGCTCACGCAGGGCAGGA  
ATAGCCAGGTTCTCATATCCCAGGGGTTGAGACTTGGCTGAGAACAGCCCCCTGGAGAACA  
TGGGGTGACTGCTACCATAGGTCTGGAAGTATGAGGCTGTCCACCAACTATCCCCTTGAA  
GCAAGTTCTCTTGAAAGGAAATCTAAACAGTGCACCCCATGGCTGCCACGGAGTATAAG  
GAGGGAGAGAAAGGAGCTGAAAGTCTAGGTTTGGCCAGCTAGGTAGACTGACTTGTGAGG  
TATTTATTTATTCATTTGAGTAACAAAGCAGACAGAATACATAGCCACCATTGGTAGTAC  
ACCCCAAAAGCAAGGATGGCATGATGCTGGTGACTCAAACGTGCCTACTCATGGTGTCAA  
ATTGGCATAATCCTCTTGGAAGCTGTGTGGAAATAAGCACAGAGAAGCAGAACTCTAAT  
TGCTTAATCCACTAAACATTACTTCTGGGAATTGGCTCATCATAAATTATCCAAGAGAAA  
GCACAAAGTTATGGGCACAAAGGTTTTCCATATAATATTATTTAAAATGCTGAGAAAATG  
AAAAAATCTAAATGGTGAAATATATACTAATGCCATCTATAAATACAAACAAATAGAATG  
TTTATAGAATAATGGAACATAATAACATTATTCAAAATTGCATTTATGCTATAGTTGTCA  
AAATTGTCTCCTTATATGATACAAAACCTCATGAAAATTATGACTTTTTTTGTTTGGTTGGA  
AAGCAGAATTATGCATAAATTTCTCTTACAGTTCGATGCCCATTAGTTTTATATAACAT  
TTATTTGACACGTACTGACTTCTATCTGAGAAGAACAAACCAAAACACTCAGGCCTAAAT  
AATTAAAAACGGTCCTAATAAACTAGCAAACCAGATAAGAAAAGATGTTAATGCCCATTTCC  
CTAACTTATGTCTTAGACCAAAATTAATTCTAGATGGTTTTAAATGACAGTGTAAGT  
AAAGTATTAAAAGATTGTGTGGTCAAATATTCAATTTAAGAGCAAGGAAATTCTTATAAA  
TATAACAATAGAGGCAGAACTCATGTAAGAATAAATTGATTAGGTGGTATTAAATATTAA  
GTTCTTATGTATGTCAAAGATATCATTTTGAAATTCATCCATCTTATTGGGTATTGCAG  
GAGTTCATTCCTTTTTGTTTATAAATACTCTTCGGTCATATGAATAGTATTCAATTTGTAT  
ACTGGTTTGTGATGGACATTTGGGTGTTCCAGTTTATGGCTATTACAAATAAAGCTT  
CTATGAACATTTATGTACA





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## FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG  
 CGGAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG  
 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCG  
 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCA  
 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT  
 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC  
 CGGGTACACCTGGGATCCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGGAATGCTCTGA  
 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGA  
 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA  
 GTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC  
 AGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTA  
 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT  
 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG  
 TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC  
 GCATCATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTTGCTACCTCTTTTT  
 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT  
 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAA  
 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT  
 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT  
 TTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTGTAC  
 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA

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## FIGURE 246

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
GVPGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDL  
GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAI IYLDQ  
GSPMNSTINIHR TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRI IIEE  
LPK

**Signal peptide:**  
amino acids 1-30

**Transmembrane domain:**  
amino acids 195-217

## FIGURE 247

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGC  
GGCGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGG  
CCCACGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACC  
ATGTGAACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCG  
ACTGGAGCGACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGG  
AGAAGCTGGACCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGA  
AGATGTACTTCCCCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGC  
ACCTCATCCAGAACGCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGC  
AGCTCTCCAGGGAGGGACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGG  
ACCTCCCCTAAGTAGCCCCCAGAGGGCGCTGGGAGTGTGTCACCGCCCTCCCCTGAAGTT  
TGCTCCATCTCACGCTGGGGGTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACAC  
ATACATGAAAACCAGGCCGCATCGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGA  
CCATCTCCTGCAACAACCTGCACAGACTCGCAGCTCGCCTGCTTTGGCTATAACTGCGAGT  
AGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTC  
TCCTTGAGGGGGCTCCCCGCCTTCCACCTGGCTGTTCATCGGGTAGGGCGGGGCCGTGGG  
TTCAGGGGCGCACCCTTCCAAGCCTGTGTCCCACAGGTCCCTCGGCGCAGTGGAAGTCAG  
CTGTCCAGGGCCTCCTGAACCTACATAAATAACTGGCACAAGTAAGTCCCCCTCCTCAAACC  
AACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGGGCACAGGCTG  
GCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACCCAGCTC  
TGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCCTCAGCTGGAGG  
CGGGCATCTTTCTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCCAGGTCTGTGG  
TCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCC  
CCACATTGCCTTTTACAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCA  
GGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGC  
ACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCAC  
ACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACAC  
ACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGC  
TCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGCACGAGG  
GTGTCGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGG  
CCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCC  
GCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCA  
ACGTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTG  
CTGCCTCAGGACCCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGC  
GGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAG  
CTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

Signal peptide:  
amino acids 1-15

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## FIGURE 249

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCC  
TGGCTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGG  
TGGCCTCGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCG  
TGCTATTGTCGGGCCCCGAGGCTCCGTGGCGGGACCTTGAGCTGCTGGAGGGGACCTGCA  
CCCCGGTGACGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGA  
TCCGCAAGCTGAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGG  
CTAGTAGTACCGGCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCCTTTGTGGTACG  
CGGACTGGATGGACGGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGC  
TGCGTCTGGCCTCGCTCTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGC  
TCATCACCAAGTTCCAAGCACCGCTGCATGGATAGCAGCGCCGCTTCTGCGAGGGGCTGT  
GGCAGCACTACCACCTGGCTTGCCGCCCGCGGACGTGCGAGATATGGAGTTTGGACCTC  
CAACAGTTAATGATAAACTAATGAGATTTTTTTGATCACTGTGAGAAGTTTTTAAGTGAAG  
TAGAAAAAATGCTACAGCTCTTTATCACGTGGAAGCCTTCAAACTGGACCAGAAATGC  
AGAACATTTTTAAAAAAGTTGCAGCTACTTTGCAAGTGCCAGTAAATGATTTAAATGCAG  
ATTTAATTCAAGTAGCCTTTTTTACCTGTTTCAATTTGACCTGGCAATTAAGGTGTTAAAT  
CTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAGAATATTTAAATGATC  
TGAAACAATATTGGAAGAGGATATGGGTATACTATTAACAGTCGATCCAGCTGCACCT  
TGTTTCAGGATATCTTTCAGCACTTGACAAAGCAGTTGAACAGAAACAAAGGTCTCAGC  
CAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTTCCACTGCTTT  
CTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAACAAA  
TGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGTGC  
TTTACCCTGTGAAAATGCTAAGACTCCTAAAGAACAATTCCGAGTGCAGATGTTATTAA  
ATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTTATGAAGATCTGA  
AGAACCCTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGAATGTGAATTAGCAA  
GGGCTAACAGTACATCTGATGAACTATTGAGTAAGTGAAGAATTTTTTAATTCTTTAGGA  
ATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCT  
TTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTCTCTGGGT  
TGGACATGAAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAAT  
CTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCTTCCTACTTAT  
ATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAAAGTGCTGG  
AGTAACAAAATATCTCAGTTGGACCATCCTTAAGTTGATTGAACTGTCTAGGAACCTTAC  
AGATTGTTCTGCAGTTCTCTCTTCTTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAA  
TCAGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGA  
GAATTTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAA  
GTACAATGAAAATAAATATTTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAAT  
AATTCCTTTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGAC  
AATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACT  
TTTTTCAATCTGTCACTTGGCTTCGATTTTTTATATTTTCTATTATGAAATGTATCTTT  
TGGTTGTTTGATTTTTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTG  
AAAGTATTTGCTATAATAAGAAAATTTCTTGTGACTTTAAAAA

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## FIGURE 250

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVL  
 LSGPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGAS  
 STGSRDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLI  
 TSSKHRCMDSSAAFLQGLWQHYHPGLPPPVDADMEFGPPTVNDKLMRFFDHCEKFLTEVE  
 KNATALYHVEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKGVKSP  
 WCDVFDIDDAKVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPI  
 SSPVILQFGHAETLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLY  
 HCENAKTPKEQFRVQMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARA  
 NSTSDEL

### Important features:

#### Signal sequence

amino acids 1-30

#### N-glycosylation sites:

amino acids 242-246, 481-485

#### N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

#### Endoplasmic reticulum targeting sequence:

amino acids 484-489

CGGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGG  
TGGCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCT  
CAGGGACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGGA  
GCCGGGGCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGCG  
GCGCTTGGGCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATC  
TTCGTGGCAAATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACT  
GGCGGGTTGACCTCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCG  
TTTTTCCACTACTCCCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGA  
ATCAGCTGGGCTGGAGACCTTGACAAGAAAGATGCATCAATCAACATAGAAAAATATGCAG  
TTTATACACAATGGCACCTATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAG  
CCTGGACACATTAGGCTCTATGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGG  
GTAGTGGTGGGCATAGTTACTGCTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATT  
CTGGCTGTCTCTATAGAAGGAAAACTCTAAACGGGATTACACTGGCTGCAGTACATCA  
GAGAGTTTGTCAACCAGTTAAGCAGGCTCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTT  
GTAAAGAGTCTGCCTTCTGGATCTCACCAGGGCCCAGTCATATATGCACAGTTAGACCAC  
TCCGGCGGACATCACAGTGACAAGATTAAACAAGTCAGAGTCTGTGGTGTATGCGGATATC  
CGAAAGAATT**TAA**GAGAATACCTAGAACATATCCTCAGCAAGAAACAAAACCAAACCTGGAC  
TCTCGTGCAGAAAATGTAGCCCATTAACCATGTAGCCTTGGAGACCCAGGCAAGGACAA  
GTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAATATTCT  
ATTTAGTCATCCTGATATGAGGAGCCAGTGTGTCATGATGAAAAGATGGTATGATTCTAC  
ATATGTACCCATTGTCCTTGCTGTTTTTGTACTTTCTTTTCAGGTCAATTACAAATGGGAG  
ATTTTCAGAAACATTCTTTTACCATCATTTAGAAATGTTTTGCCTTAATGGAGACATAAG  
CAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAGGGCTTAAGACTGATTA  
GTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATAACCAGGGTG  
GCCTTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTTAAAAAATACCCATTGG  
CTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTTCTCACTAAAATATGGG  
GCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTTGCAACCCTTGAAATGTGT  
CATATCAATTTCTGGATTACATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCACT  
TCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTTGAGA  
ACTTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA



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## FIGURE 252

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKF  
KSTSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASI  
NIENMQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLT  
LLISMILAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVI  
YAQLDHSGGHHSDKINKSESVVYADIRKN

**Signal peptide:**  
amino acids 1-37

**Transmembrane domain:**  
amino acids 161-183

## FIGURE 253

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCT  
CGAGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTC  
CTGCTCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCC  
GGGACTGGTGC GCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTG  
GGGCTGCTGCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCCGAAGCGGGGC  
TCACTGCTCTGGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAG  
GAGGAGCGGGGCCGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATC  
CCAAGGCGACCCGGGGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCT  
CCTGCGTGCTCCCTGGTGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTG  
GCCGGCAACGTGGTGGGCGTGTCCGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAG  
GTGGAGGACGTGGACCTGGAGCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACA  
GCCCCAGGCCCTGAGACGGCGGCCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAG  
GCCAAGAACCCCCAGGAGCAGAAGTCCTTCTTCGCCAAATACTGGATGTACATCATTTCCC  
GTCGTCCTGTTCCCTCATGATGTCAGGAGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGG  
GGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCACCCTCCCTGTAAAGTCTAT  
TTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTTGAAAAGCTACAGCTTCCAGC  
AGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCTGATGTACAAGCTTGATTGAAATTC  
ACTGCTCACTTGATACGTTATTCAGAAACCCAAGGAATGGCTGTCCCCATCCTCATGTGG  
CTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCCAGATCGACACG  
CAAAAAAAAA

## FIGURE 254

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSF  
EIDDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRPGALD  
GLEAGGYVSSFVPACSLVESHLSLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLEL  
FNTSVQLQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMS  
GAPDTGGQGGGGGGGGGGGSGLCVPPSL

**Signal peptide:**  
amino acids 1-24

**Transmembrane domain:**  
amino acids 226-243

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## FIGURE 255

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGA  
TGGTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGG  
CCCACGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTC  
GATACATCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATG  
AGCAGATTACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTT  
TCTTCATCCAGGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGA  
CTCGGGTGGTCCAGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACA  
ATGACAGCTTCTACGTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCG  
CCCTCTTCCTGCTCGGCCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGC  
TGCCATGGGCCATCATTTCCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGC  
TGCAACCGCCCTGGACCTTCTGGTAGAAAGAGTTTGTCCCACATTCCAGCCATAAGTGACT  
CTGAGCTGGGAAGGGGAAACCCAGGAATTTTGCTACTTTGGAATTTGGAGATAGCATCTGG  
GGACAAGTGGAGCCAGGTAGAGGAAAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCC  
ACACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGC  
AAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAAAGGAGCTGAAGGCAGGTG  
GCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCCTCCCCTACCCAGGGT  
CTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCTGGTGTTTGGGGA  
CTCAATAAACCTCACTGACTTTTTTAGCAATAAAGCTTCTCATCAGGGTTGCAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

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## FIGURE 256

MVPGAAGWCCLVLWLPACVAAHGFRIHLYFQVLSPGDIRYIFTATPAKDFGGIFHTRY  
EQIHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDनाव  
NDSFYVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFEL  
LQPPWTFW

**Signal peptide:**  
amino acids 1-20

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## FIGURE 257

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGG  
 AGGGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCA  
 GAGGCCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAG  
 ATGTATGGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATC  
 ACAGGGCTGCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGA  
 GACTCCTGGGACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAG  
 CCAGGCGAATACATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTC  
 ATGTACACCAGCAAGGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCT  
 GCCTACCCCAGCCAAGAGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTT  
 GGCATCAAGAGCATTGGCTTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCA  
 CCAGTTAATCTCACATACTCAGCAAACACCCGTGGGTCGCTTAGGGGTGGGGTATGGGGC  
 CATCCGAGCTGAGGCCATCTGTGTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGG  
 ACGCTGAATCTGAATCCACCAATAAATAAAGCTTCTGCAGAAAA

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## FIGURE 258

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQ  
VKLGDSWDVKLGALGGNTQEVTLQPGEYITKVVFVAFQAFLRGMVMTSKDRYFYFGKLDG  
QISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**  
amino acids 1-22

## FIGURE 259

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCC  
CCAGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGA  
AGATTCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCA  
TCCCAGCTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAA  
AGGAGCTCTGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAAC  
CAGCCCAGGGCTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCT  
CCAAAGGCTGCAAGAGGACTGAGCGGTACAGACCCCTAAAGGGCCATAGCCCCAGTGAGC  
AGCCTGGAGCCCTGGAGACCCCACCAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATG  
CAAGAAGGAGGCTATGCTCAGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACAC  
TCTTTCTCCTGCTTTAACCACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCT  
GCCCACAGCAGGCCAGGTCCAGAGAGACCGAGGAGGGAGAGTCTCCAGGGAGCATGAGA  
GGAGGCAGCAGGACTGTCCCCTTGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCT  
CCCCAGTACACCCACCTCTTCCTTGTAATATGATTTATACCTAACTGAATAAAAAGCT  
GTTCTGTCTTCCCNCCCA





GGGACTACAAAGCCGCGCGCTGCGCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGA  
GGCGGCCACCGCGACTCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTT  
TCAGGGGCTGCCTGATAGGGGCTGTAAATCTCAAATCCAGCAATCGAACCCCAAGTGGTAC  
AGGAATTTGAAAGTGTGGAACGTCTTGCATCATTACGGATTCGCAGACAAGTGACCCCA  
GGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGTCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGA  
ATGTGACACGGAGAGACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCA  
AGGAAATTGATGAGATTGTGATCGAGTTAACTGTGCAAGTGAAGCCAGTGACCCCTGTCT  
GTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGCACTGCCAGGAGAGTG  
AGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACTT  
TGGTGTTCACTGCTGTTTACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATG  
ACGCAGGCTCAGCCAGGTGTGAGGAGCAGGAGATGGAAGTCTATGACCTGAACATTGGCG  
GAATTATTGGGGGGGTTCTGGTTGTCTTGTCTGTACTGGCCCTGATCACGTTGGGCATCT  
GCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGAC  
ACAAGTCATCGTTTGTGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGT  
GCACATACCTCTGCTAGAAACTCCTGTCAAGGCAGCGAGAGCTGATGCACTCGGACAGAG  
CTAGACACTCATTCAGAAGCTTTTCGTTTTTGGCCAAAGTTGACCACTACTCTTCTTACTC  
TAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTTCTGGCCTGATTCC  
CGCATGAGTATTAGGGTGATCTTAAAGAGTTTGTCTCACGTAAACGCCCGTGCTGGGCCCT  
GTGAAGCCAGCATGTTCACTACTGGTTCGTTTCAGCAGCCACGACAGCACCATGTGAGATGG  
CGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCAGAAAAGGCTTCTTAC  
ACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTTTGTAAAAACA  
ACCAAATCAGGAAGGTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCCCTGCT  
TGTCCAACAGGGTGTGAGGATTTAAGGAAAACCTTCGTCTTAGGCTAAGTCTGAAATGTT  
ACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTTTACATCTAAATTTT  
GCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTTAAAAAAGTTCAACTTAAAGGTAGAAGTTCCAAG  
CTACTAGTGTTAAATTGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCT  
CATGGAAGTTTACTGTGATGTTCTCTTTTCTACACAAGTTTTAGCCTTTTTTCACAAGGGA  
ACTCATACTGTCTACACATCAGACCATAGTTTGCTTAGGAAACCTTTTAAAAATTCCAGTTA  
AGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGAT  
GTACATACACAGATGCCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCA  
CTGTTGCCTCGCTGTCTGCCAGGAGGCCCTGCCATCCTTGGGGCCCTGGCAGTGGCTGTGT  
CCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGCTCTCAGGTGGGCACT  
GCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTTTAAGTTT  
GTTTAATTATTTGTTAAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAA  
GTACAATAACATTTTAAAAAGAAAATGGATCCCACTGTTTCTTCTTTGCCACAGAGAAAGC  
ACCCAGACGCCACAGGCTCTGTGCAATTTCAAAACAAACCATGATGGAGTGGCGGCCAGT  
CCAGCCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAAGCAGTTTTTCTAATTTTGACTTTAAATTTTTTCATCCGCCGA

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GACACTGCTCCCATTTGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCA  
 AGAGCAGGTGTTCTCAGCCTCACATGCCCTGCCGTGCTGGACTCAGGACTGAAGTGCTGT  
 AAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGAGAATGGCTCTCACTA  
 CTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT  
 AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGCAGGC  
 CGCCTGGCAGAGGCAGGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCA  
 TGGCATCCTGGATGCTTAGCATGCAAGTTCCCTCCATCATTGCCACCTTGGTAGAGAGGG  
 ATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCTTCTTGGTTGTCATAG  
 TGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA  
 TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCT  
 ATAAGTGAAGTCTGAGACTAGACGGAAAAGGAATACTCGTGTATTTTAAGATATGAATGTGACTCAA  
 GACTCGAGGCCGATACGAGGCTGTGATTCTGCCTTTGGATGGATGTTGCTGTACACAGAT  
 GCTACAGACTTGTAATAACACACCGTAATTTGGCATTTGTTTAACCTCATTTATAAAAGC  
 TTCAAAAAAACCCA

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## FIGURE 262

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT  
SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS�KIWNVTRRDSALYRCEVVAR  
NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL  
PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDL  
NIGGIIGGVLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG  
DFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites:**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 107-110

**Casein kinase II phosphorylation site:**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site:**

amino acids 69-77

**N-myristoylation sites:**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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# FIGURE 265

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCCTGGTCGGGGTGGTCTGTCTGC  
 TCCTGGCATGCCCTGCCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCA  
 CCCTGGGTCTGTGTGCGAGGCCGGCAGGTGGGCGTGAAGGGCACAGACCGCCTTGTGAATG  
 TCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACCGTTCTCAGCCCCAC  
 ACCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC  
 AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAACAGCAGATCTTCT  
 CCGTTTCAGAGGACTGCCTGGTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGCAGGGT  
 CCGGTAGGCCGGTTCATGGTATGGGTCCATGGAGGCGCTCTGATAACTGGCGCTGCCACCT  
 CCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCGTGGTTACAGTCCAGTACC  
 GCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
 TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTG  
 ACCTCAACTGTGTCACTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGG  
 TCCTGTCCCCAGTGGCTGCAGGGCTGTTCCACAGAGCCATCACACAGAGTGGGGTTCATCA  
 CCACCCAGGGATCATCGACTCTCACCCTTGGCCCCCTAGCTCAGAAAATCGCAAACACCT  
 TGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
 AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCA  
 CTGTCTTCCCCAAAAGCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCT  
 TCCTCATGGGTGTCAACAACCATGAGTTCAGCTGGCTCATCCCCAGGGGGCTGGGGTCTCC  
 TGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCTCAACACCCGTCTTGA  
 CCAGTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA  
 ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCA  
 ATGTTCCCACCGTCAGTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCT  
 ATGAGTTCAGCATCGACCCAGTTCTTTTGCGAAGATCAAACCTGCCTGGGTGAAGGCTG  
 ATCATGGGGCGAGGGTGCTTTTGTGTTCCGAGGTCCCTTCCTCATGGACGAGAGCTCCC  
 GCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAGCAAGCCTCACCATGATGGCCC  
 AGTGGACCCACTTTGCCCCGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCC  
 AATTCAACCAGGCGGAACAATATCTGGAGATCAACCCAGTGCCACGGGCCGGACAGAAGT  
 TCAGGGAGGCCTGGATGCAGTTCTGGTCAGAGACGCTCCCCAGCAAGATACAACAGTGGC  
 ACCAGAAGCAGAAGAACAGGAAGGCCCAGGAGGACCTCTGAGGGCCAGGCCTGAACCTTCT  
 TGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC  
 CCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAG  
 TTATGCTCTTTTGAAATGTCACAAGGCCGCCTCCACCTCTGGGGCATTGTACAAGTTCT  
 TCCCTCTCCCTGAAGTGCCTTTCTGCTTTCTTCGTGGTAGGTTCTAGCACATTCCTCTA  
 GCTTCCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTCTGGGCTGTGCGGCC  
 CGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT  
 CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTCAACCCACAC  
 CAGGATCGGGTGGGACCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGA  
 ATATGGGAATGGCAGCTGCTGAACTTGAACCCAGAGCCTTCAGGTGCCAAAGCCATACTC  
 AGGCCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCCAATGGCAGAGACCTG  
 GGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCCTGAC  
 TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGTGCTGCCCAGTCTGGCCCCCT  
 GCACAAGACAACAGAATCCATCAGGGCCATGAGTGTCAACCCAGACCTGACCTCACCAT  
 TCCAGCCCCCTGACCTCAGGACGCTGGATGCCAGCTCCCAGCCCCAGTGCCGGGTCTCTCC  
 CTCCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAGAGCACCCACCAAGAC  
 ACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGCGGGCTATTGTACACA  
 GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGGTTTTCT

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AGATGGAAGTGAGAGGTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGCTCTCCCT  
 GCCGCCTCTGCCTGGGCTCCCACTTTGGCAGCACTTGAGGAGCCCTTCAACCCGCCGCTG  
 CACTGTAGGAGCCCCCTTCTGGGCTGGCCAAGGCCGAGCCAGCTCCCTCAGCTTGCGGG  
 GAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG  
 AGTGAGTTCGGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCC  
 AGGCAGTGAGGGCCTTAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCC  
 TTAGCTGCCCTCCCCGCGGGGCAGGGCTCGGGACCTGCAGCCCTCCATGCCTGACCCCTCCC  
 CCCACCCCCCGTGGGCTCCTGTGCGGCCGAGCCTCCCCAAGGAGCGCCGCCCCCTGCTC  
 CACAGCGCCCAGTCCCATCGACCACCCAAGGGCTGAGGAGTGCGGGGTGCACAGCGCGGGA  
 CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGCTGGATCCACTGGGTGAAGCCAGCTGGGC  
 TCCTGAGTCTGGTGGGGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACAC  
 CGATGGGCACTCTGTATCTAGCTCAAGGTTTGTAAACACACCAATCAGCACCCCTGTGTCT  
 AGCTCAGTGTTTGTGAATGCACCAATCCACACTCTGTATCTGGCTACTCTGGTGGGGACT  
 TGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
 TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCCTGTCAAAACAGACCACTT  
 GACTCTCTGTAAAATGGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAA  
 GCAGGCTGCCTGAGCCAGCAGTGACAACCCCCCTCGGGTCCCCTCCCACGCCGTGGAAGC  
 TTTGTTCTTTCGCTCTTTGCAATAAATCTTGCTACTGCCCAAAA



## FIGURE 266

MERAVRVESGVLVGVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGVKGTDRLVNVF  
 LGIPFAQPPLGPDRFSAPHPAQFWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSV  
 SEDCLVLNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAGDVVVVTVQYRL  
 GVLGFFSTGDEHAPGNQGFLDVVAALRWVQENIAPFGDLNLCVTVFSGSAGGSIISGLVL  
 SPVAAGLFHRAITQSGVITTPGIIDSHPWPLAQKIANLTLACSSSSPAEMVQCCLQQKEGEE  
 LVLSKKLKNTIYPLTVDGTVPFKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLD  
 TMEQMSREDMLAISTPVLTSLDVPPPEMMPTVIDEYLGNSDAQAKCQAFQEFMGDVFINV  
 PTVSFSRYLRDSGSPVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRL  
 AFPEATEEEKQLSLTMMAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFR  
 EAWMQFWSETLPSKIQWHQKQKNRKAQEDL

### Important features of the protein:

#### Signal peptide:

amino acids 1-27

#### Transmembrane domain:

amino acids 226-245

#### N-glycosylation site:

amino acids 105-109

#### N-myristoylation sites:

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
 162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
 461-467

#### Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 12-23

#### Carboxylesterases type-B serine active site:

amino acids 216-232

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## FIGURE 267

TGTCGCCTGGCCCTCGCC**ATG**CAGACCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTG  
CTTCTGCTGCTGCTACTGGGGGCGCCACGGCCTCTTTCCTGAGGAGCCGCCGCCGCTT  
AGCGTGGCCCCCAGGGACTACCTGAACCACTATCCCGTGTTTGTGGGCGAGCGGGCCCGGA  
CGCCTGACCCCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGAGTCTTGCGGGTCAAC  
AGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCACG  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAAC  
GTGTGTCGGATGAAGGGCAAACAGGAGGGCGAGTGTCGAAACTTCGTAAAGGTGCTGCTC  
CTTCGGGACGAGTCCACGCTCTTTGTGTGCGGTTCCAACGCCTTCAACCCGGTGTGCGCC  
AACTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGCGGTATGGCCCGCTGC  
CCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTACAGCT  
ACTGTTACCGACTTCCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCC  
ACCCTGCGCACCGTGAAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCG  
GTGGAGTGGGGCAGCCATGTCTACTTCTTCTTCCGGGAGATTGCGATGGAGTTTAACTAC  
CTGGAGAAGGTGGTGGTGTCCCGCGTGCGCCGAGTGTCGCAAGAACGACGTGGGAGGCTCC  
CCCCGCGTGCTGGAGAAGCAGTGGACGTCTTCTGTAAGGCGCGGCTCAACTGCTCTGTA  
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGCTCAGCCTC  
GGGGGCCCGCCCGTGGTCTTGCCGTTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCG  
GCTGTCTGCGCCTTTGACCTGACACAGGTGGCAGCTGTGTTTGAAGGCCGCTTCCGAGAG  
CAGAAGTCCCCCGAGTCCATCTGGACGCCCGGTGCCGGAGGATCAGGTGCCTCGACCCCGG  
CCCGGGTGCTGCGCAGCCCCCGGGATGCAGTACAATGCCCTCCAGCGCCTTGCCGGATGAC  
ATCCTCAACTTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCAT  
GCGCCCTGGATCCTGCGGACCTGATGAGGCACCAGCTGACTCGAGTGGCTGTGGACGTG  
GGAGCCGGCCCCCTGGGGCAACCAGACCGTTGTCTTCTTGGGTTCTGAGGCGGGGACGGTC  
CTCAAGTTCTCGTCCGGCCCCAATGCCAGCACCTCAGGGACGTCTGGGCTCAGTGTCTTC  
CTGGAGGAGTTTGAGACCTACCGGCCGGACAGGTGTGGACGGCCCCGGCGGTGGCGAGACA  
GGGCAGCGGCTGCTGAGCTTGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTC  
CCCCGCTGCGTGCTCCGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAG  
AACTGTATCGGCAGTCAGGACCCCTACTGCGGGTGGGCCCCCGACGGCTCCTGCATCTTC  
CTCAGCCCCGGGCACCAGAGCCGCCTTTGAGCAGGACGTGTCCGGGGCCAGCACCTCAGGC  
TTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG  
TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCCTTCGTGGTGGGAGCCGTGGTGTCC  
GGCTTCAGCGTGCGGTGGTTCGTGGGCCTCCGTGAGCGGCGGGAGCTGGCCCCGGCGCAAG  
GACAAGGAGGCCATCCTGGCGCACGGGGCGGGCGAGGCGGTGCTGAGCGTCAGCCGCCTG  
GGCGAGCGCAGGGCGCAGGGTCCCCGGGGGCGGGGCGGAGGCGGTGGCGGTGGCGCCGGG  
GTTCCCCCGGAGGCCCTGCTGGCGCCCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCCCGAGCAGACGCCG  
CTGCCGCAGAAGCGCCTGCCACTCCGCACCCCGCACCCCCACGCCCTGGGCCCCCCGCGCC  
TGGGACCACGGCCACCCCTGCTCCCCGCCCTCCGCTTCATCCTCCCTCCTGCTGCTGGCG  
CCCGCCCCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACCCCCGACGGCCGCCTC  
TATGCTGCCCGGCCCCGGCCGCCCTCCACGGCGACTTCCCGCTCACCCCCACGCCAGC  
CCGACCGCGCGGGTGGTGTCCGCGCCACGGGCCCCCTTGGAACCAAGCCTCAGCCGCC  
GATGGCCTCCCGCGGCCCTGGAGCCCGCCCCCGACGGGCAGCCTGAGGAGGCCACTGGGC  
CCCCACGCCCTCCCGGCCGCCACCCTGCGCCGCACCCACACGTTCAACAGCGGCGAGGCC  
CGGCCTGGGGACCGCCACCGCGGCTGCCACGCCCGGGCGGGCACAGACTTGGCCACCTC  
CTCCCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGCCCT**TAG**GCGGGGGCCCCCG  
ATGCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAACGCCGGGG  
CCCGGGGCAACTCCGAGTGGGTGCTCAAGTCCCCCCCCGCGACCCACCCGCGGAGTGGGGG

GCCCCCTCCGCCACAAGGAAGCACAAACCAGCTCGCCCTCCCCCTACCCGGGGCCGCAGGA  
CGCTGAGACGGTTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATGGATTTGAGGTTGACC  
TTATGCGCGTAGGTTTTTGGTTTTTTTTTTGCAGTTTTTGGTTTTCTTTTGGGTTTTCTAACC  
AATTGCACAACCTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGGACGCCGGTGGGG  
AATGGGGGGGCCACAGCTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCA  
ACCCAGGCCCTTGGCGTGTGTGGGTGTGCGTGCGTGCGTGCCGTGTTTCGTGTGCAAGG  
GGCCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTGTGGGCGTGTGTGTCA  
AGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGGTCTCCGAGGTGCCG  
GTTAGGAGTTTGAACCCCCCCCCACTCTGCAGAGGGAAGCGGGGACAATGCCGGGGTTTCA  
GGCAGGAGACACGAGGAGGGCCTGCCCGGAAGTCACATCGGCAGCAGCTGTCTAAAGGGC  
TTGGGGGCCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAAATACGGCCCCAGGGT  
GGTGAGAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCTCCCCCAGC  
CCCCCTCCCCATCAATAAAACTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



FIGURE 269

ATCTGAGTGAGCTAACTGACACAATGAACTGTCTAGGCATGTTTCTGCTCCTCTCTCTGG  
CTCTTTTCTGCTTTTTTAACAGGTGTCTTCAGTCAGGGAGGACAGGTTGACTGTGGTGAGT  
TCCAGGACCCCAAGGTCTACTGCACTCGGGAATCTAACCACACTGTGGCTCTGATGGCC  
AGACATATGGCAATAAATGTGCCTTCTGTAAGGCCATAGTGAAAAGTGGTGAAAGATTA  
GCCTAAAGCATCCTGGAAAATGCTGA GTTAAAGCCAATGTTTCTTGGTGACTTGCCAGCT  
TTTGCAGCCTTCTTTTCTCACTTCTGCTTATACTTTTGCTGGTGATTCTTTTAATTCAT  
AAAGACATACCTACTCTGCCTGGGTCTTGAGGAGTTCAATGTATGTCTATTTCTCTTGAT  
TCACTTGTCAATAAAGTACATTCTGCAAAGCAAAA

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## FIGURE 270

MKLSGMFLLLSLALFCFLTGVFSQGGQVDCGEFQDPKVYCTRESNPHCGSDGQTYGNKCA  
FCKAIVKSGGKISLKHPGKC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites:**

amino acids 26-32, 52-58, 56-62, 69-75

**Kazal serine protease inhibitors family signature:**

amino acids 40-63

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## FIGURE 271

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTAC  
 ACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTT  
 GCCCCGGAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCCAGAATTCCA  
 GTTCTGGTTTTCATGCCAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCA  
 TTTAAGAGGGTTTTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCAT  
 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGCTTGAAATGAGGAAC TGAGAAAATT  
 AATTTCTCATGTATTTTTCTCATTTATTTATTAATTTTTAACTGATAGTTGTACATATTT  
 GGGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAAATCAGGGTAAC  
 TGGGATATCCATCACATCAAACATTTATTTTTTATTCTTTTTTAGACAGAGTCTCACTCTG  
 TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT  
 TCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAAT  
 GCCCAACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGGCTGGC  
 CTTGAACTCCTGGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACA  
 GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAACTTTGAA  
 ATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACT  
 TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTC  
 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCAC  
 TTTTCTAGCTCCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTA  
 TTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGATTTTCGT  
 TCTTAATTTCAATTAAAATAACCACACATGGCAAAAA

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## FIGURE 272

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRVSVAREHLPSRGSLLRGPRPRIPLV  
SCQPVKGHGTGESPMPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:  
amino acids 1-18

N-myristoylation site:  
amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature:  
amino acids 68-79



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## FIGURE 273

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCG  
CAGCCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTC  
TATCAGTTATGGCTAAATCCTGTCCATCTGTGTGTGCTGCGATGCGGGTTTCATTACT  
GTAATGATCGCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCT  
ACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCTTCAGATTTGAAAACTTGCTGA  
AAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTCCTACCAACCTCCCAA  
AGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCAC  
TTTCAAAAATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTA  
GCATAGAAGAGGGAGCATTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTA  
ATCACCTTAGCACAAATTCCTGGGGTTTGCCAGGACTATAGAAGAACTACGCTTGGATG  
ATAATCGCATATCCACTATTTTCAACCATCTCTTCAAGGTCTCACTAGTCTAAAACGCC  
TAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCTGACTGCTGCACCAGTAAACC  
TTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCC  
CAAATGGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAA  
GTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACACAACCTGATTCTTCGCA  
ACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGTTACAATCACTAC  
CTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTCTGTGGGATGG  
CTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGCACCA  
TTCAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTC  
CAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG  
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTC  
ATATCTCTTGGAACCTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAACTGG  
GCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGT  
ACTTGGTCACAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTCCCATGGAAA  
CCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCC  
TTCGAATGTACAACCTTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAA  
ACCCCAATTTACCTTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCC  
TTCTTGCTTTAGTGTGTTGGTATGTTTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTG  
CATATAGCAAAGGGAGGAGAAGAAAGGATGACTATGCAGAAGCTGGCACTAAGAAGGACA  
ACTCTATCCTGGAAATCAGGGAAACTTCTTTTCAGATGTTACCAATAAGCAATGAACCCA  
TCTCGAAGGAGGAGTTTGTAAATACACCATATTTCTCCTAATGGAATGAATCTGTACA  
AAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACT  
CAGATCACTCACACTCATGATGTCTGAAGGACTCACAGCAGACTTGTGTTTGGGTTTTTT  
AAACCTAAGGGAGGTGATGGT

## FIGURE 274

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLT SIPTGI PEDAT  
 TTLYLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRITIT  
 YDSLSKIPYLEELHLDNSVSAVSIEEGAFRDSNYLRLFLSRNHLSTIPWGLPRTIEEL  
 RLDDNRISTISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAA  
 PVNLPGTNLRKLYLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDLDNITQL  
 ILRNNPWYCGCKMKWVRDWLQSLPVKVNVRGLMCQAPKVRGMAIKDLNAELFDCKDSGI  
 VSTIQITTAIPNTVYPAQGQWPAPVTKQPD IKNPKLT KDQQT TGSPSRKTITITVKS VTS  
 DTIHISWKLALPMTALRLSWLKLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVC MV  
 PMETSNLYLFDETPVC IETETAPLRMYNPTTTLNREQEKEPYKNPNLPLAAIIGGAVALV  
 TIAL LALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNSILEIRETSFQMLPIS  
 NEPISKEEFVIHTIFPPNGMNLYKNNHSESSNRSYRDSGIPDSDHSHS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites:**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site:**

amino acids 515-522

**N-myristoylation sites:**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561, 640-645

**Amidation site:**

amino acids 567-570

**Leucine zipper pattern:**

amino acids 159-180

**Phospholipase A2 aspartic acid active site:**

amino acids 34-44

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## FIGURE 275

AGGGCCCGCGGGTGGAGAGAGCGACGCCCCGAGGGG**AT**GGCGGCAGCGTCCCGGAGCGCCT  
 CTGGCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGCCGGCTCCGGCG  
 TCTTCCAGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGGCGTACTGGCCAGTGGGCGGC  
 CTTGCGAGCCCCGGCTGCCGGAATTTCTTCCGCGTCTGCCTTAAGCACTTCCAGGCGGTG  
 TCTCGCCCCGACCTTGACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCT  
 TCGCTGTCCGGGACGACAGTAGCGGCGGGGGGCGCAACCCTCTCCAAGTGGCCCTTCAATT  
 TCACCTGGCCGGGTACCTTCTCGCTCATCATCGAAGCTTGGCACGCGCCAGGAGACGACC  
 TGGCGCCAGAGGCCTTGCCACCAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCC  
 TAGCTGTGGGTGAGAACTGGTTATTGGATGAGCAAACCAGCACCTCACAAGGCTGCGCT  
 ACTCTTACCGGGTCACTGTCAGTGACAATACTATGGAGACAAGTGGTCCCGCTGTGCA  
 AGAAGCGCAATGACCACTTCGGCCACTATGTGTGCCAGCCAGATGGCAACTTGTCTGCGC  
 TGCCCCGTTGGACTGGGGAATATTGCCAACAGCCCTATCTGTCTTTCGGGCTGTGATGAAC  
 AGAATGGCTACTGCAGCAAGCCAGCAGAGTGCCCTTGCCTGCCAGGCTGGCAGGGCCGGC  
 TGTGTAACGAATGCATCCCCCACAAATGGCTGTGCGCACGGCACCTGCAGCACTCCCTGGC  
 AATGTACTTGTGATGAGGGCTGGGGAGGCCTGTTTTGTGACCAAGATCTCAACTACTGCA  
 CCCACCACTCCCCATGCAAGAATGGGGCAACGTGCTCCAACAGTGGGCAGCGAAGCTACA  
 CCTGCACCTGTGCGCCAGGCTACACTGGTGTGGACTGTGAGCTGGAGCTCAGCGAGTGTG  
 ACAGCAACCCCTGTGCAATGGAGGCAGCTGTAAGGACCAGGAGGATGGCTACCACTGCC  
 TGTGTCTCCGGGCTACTATGGCCTGCACTGTGAACACAGCACCTTGAGCTGCGCCGACT  
 CCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAACCAGGGGGCCAATATGCTTGTG  
 AATGTCCCCCAACTTCACCGGCTCCAAGTGCAGAGAAGAAAGTGGACAGGTGCACCAGCA  
 ACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAAGCCGCATGTGCCGCTGCC  
 GTCCTGGATTACAGGGCACCTACTGTGAATCCACGTCAGCGACTGTGCCCCGTAACCCTT  
 GCGCCACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTGCACCTGCCCTGCCG  
 GCTTCTCTGGCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTGCCTCGAGTCCCT  
 GCTTCAACAGGGCCACCTGCTACACCGACCTCTCCACAGACACCTTTGTGTGCAACTGCC  
 CTTATGGCTTTGTGGGCAGCCGCTGCGAGTTCCCCGTGGGCTTGCCGCCAGCTTCCCCCT  
 GGGTGGCCGTCTCGCTGGGTGTGGGGCTGGCAGTGCTGCTGGTACTGCTGGGCATGGTGG  
 CAGTGGCTGTGCGGCAGCTGCGGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCCATGA  
 ACAACTTGTGCGACTTCCAGAAGGACAACCTGATTCCTGCCGCCAGCTTAAAAACACAA  
 ACCAGAAGAAGGAGCTGGAAGTGGACTGTGGCCTGGACAAGTCCAAGTGTGGCAAACAGC  
 AAAACCACACATTGGACTATAATCTGGCCCCAGGGCCCCCTGGGGCGGGGGACCATGCCAG  
 GAAAGTTTCCCCACAGTGACAAGAGCTTAGGAGAGAAGGCGCCACTGCGGTTACACAGTG  
 AAAAGCCAGAGTGTGCGATATCAGCGATATGCTCCCCCAGGGACTCCATGTACCAGTCTG  
 TGTGTTTGTATATCAGAGGAGAGGAATGAATGTGTGATTGCCACGGAGGTAT**TA**AGGCAGGA  
 GCCTACCTGGACATCCCTGCTCAGCCCCGCGGCTGGACCTTCCTTCTGCATTGTTTACA

## FIGURE 276

MAAASRSASGWALLLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRV  
 CLKHFQAVVSPGPCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIE  
 AWHAPGDDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQTSTLTRLRYSYRVICSDNY  
 GDNC SRLCKKRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECL  
 CRPGWQGRLCNECIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATC  
 SNSGQRSYTCTCRPGYTGVDCLELSECDNPNCRNGGSCKDQEDGYHCLCPPGYGLHCE  
 HSTLSCADSPCFNGGSCRERNQGANACECPNFTGSGNCEKKVDRCTSNPCANGGQCLNR  
 GPSRMCRCRPGFTGTCELVSDCARNPCAHGGTCHDLENGLMCTCPAGFSGRRCEVRTS  
 IDACASSPCFNATCYTDLSTDTFVCNCPYGFVGSRCFVGLPPSFPWVAVSLGVGLAV  
 LLVLLGMVAVVRQLRLRRPDDGSREAMNLSDFQKDNLI PAAQLKNTNQKKELEVDCGL  
 DKSNCGKQQNHTLDYNLAPGPLGRGTM PGKFP HSDKSLGEKAPLRLHSEKPECRISAICS  
 PRDSMYQSVCLISEERNECVIATEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 530-552

**N-glycosylation sites:**

amino acids 108-112, 183-187, 205-209, 393-397, 570-574,  
 610-614

**Glycosaminoglycan attachment site:**

amino acids 96-100

**Tyrosine kinase phosphorylation site:**

amino acids 340-347

**N-myristoylation sites:**

amino acids 42-48, 204-210, 258-264, 277-283, 297-303,  
 383-389, 415-421, 461-467, 522-528, 535-541, 563-569,  
 599-605, 625-631

**Amidation site:**

amino acids 471-475

**Aspartic acid and asparagine hydroxylation site:**

amino acids 339-351

**EGF-like domain cysteine pattern signature:**

amino acids 173-185, 206-218, 239-251, 270-282, 310-322,  
 348-360, 388-400, 426-438, 464-476, 506-518

**Calcium-binding EGF-like:**

amino acids 224-245, 255-276, 295-316, 333-354, 373-394,  
 411-432, 449-470

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## FIGURE 277

GGCAGTGCAGCCGCCTCACAGGTGCGCGGACGGGCCAGGCGGGCGGCCTCCTGAACCGAA  
CCGAATCGGCTCCTCGGGCCGTCGTCTCCCGCCCCCTCCTCGCCCGCCCGGAGTTTTC  
TTTCGGTTTCTTCCAAGATTCTTGGCCTTCCCTCGACGGAGCCGGGCCCAGTGCGGGGGC  
GCAGGGCGCGGGAGCTCCACCTCCTCGGCTTTCCCTGCGTCCAGAGGCTGGCATGGCGCG  
GGCCGAGTACTGAGCGCACGGTGGGGCACAGCAGGGCCGGGGGGTGCAGCTGGCTCGCG  
CCTCCTCTCCGGCCGCCGTCTCCTCCGGTCCCTGGCGAAAGCCATTGAGACACCAGCTGG  
ACGTCACGCGCCGGAGCATGTCTGGGAGTCAGAGCGAGGTGGCTCCATCCCCGCAGAGTC  
CGCGGAGCCCCGAGATGGGACGGGACTTGCGGCCCGGGTCCCGCGTGCTCCTGCTCCTGC  
TTCTGCTCCTGCTGGTGTACCTGACTCAGCCAGGCAATGGCAACGAGGGCAGCGTCACTG  
GAAGTTGTTATTGTGGTAAAAGAATTTCTTCCGACTCCCCGCCATCGGTTTCAGTTCATGA  
ATCGTCTCCGGAACACCTGAGAGCTTACCATCGGTGTCTATACTACACGAGGTTCCAGC  
TCCTTTCTTGGAGCGTGTGTGGGGGCAACAAGGACCCATGGGTTCAGGAATTGATGAGCT  
GTCTTGATCTCAAAGAATGTGGACATGCTTACTCGGGGATTGTGGCCCCACCAGAAGCATT  
TACTTCCTACCAGCCCCCAATTTCTCAGGCCTCAGAGGGGGCATCTTCAGATATCCACA  
CCCCTGCCCAGATGCTCCTGTCCACCTTGAGTCCACTCAGCGCCCCACCCTCCCAGTAG  
GATCACTGTCTCGGACAAAGAGCTCACTCGTCCCAATGAAACCACCATTACACTGCGG  
GCCACAGTCTGGCAGCTGGGCCTGAGGCTGGGGAGAACCAGAAGCAGCCGGAAAAAATG  
CTGGTCCCACAGCCAGGACATCAGCCACAGTGCCAGTCTGTGCCTCCTGGCCATCATCT  
TCATCCTCACCGCAGCCCTTTCTTATGTGCTGTGCAAGAGGAGGAGGGGGCAGTACCGC  
AGTCCTCTCCAGATCTGCCGGTTCATTATATACCTGTGGCACCTGACTCTAATACTGAG  
CCAAGAATGGAAGCTTGTGAGGGTAAACTGTGGCTTATTCTTACAAAAAGTGTAATAAAG  
GAGACTGACCCCTGACAACATGGTAGGCACTGTAAAAA



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## FIGURE 280

MALLLCFVLLCGVVDFARSLSTTTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLIS  
 PADNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC  
 KVKKAPGVANKKIHLVVLVKPSGARCIVDGEIGSDFKIKCEPKESLPLQYEWQKLS  
 SQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIA  
 GAIIGTLLALALIGLIIFCCRKKRREEKYEKEVHDIREDVPPPKSRTSTARSYIGSNHS  
 SLGSMSPSNMEGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITV

**Signal sequence.**  
 amino acids 1-19

**Transmembrane domain:**  
 amino acids 236-257

**N-glycosylation sites:**  
 amino acids 106-110, 201-205, 298-302

**Tyrosine kinase phosphorylation sites:**  
 amino acids 31-39, 78-85, 262-270

**N-myristoylation sites:**  
 amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
 245-251, 296-302

**Myelin P0 protein:**  
 amino acids 96-125



# FIGURE 281

TGCATCAGTGCCCAGGCAAGCCCAGGAGTTGACATTTCTCTGCCCAGCCATGGGCCTCAC  
CCTGCTCTTGCTGCTGCTCCTGGGACTAGAAGGTCAGGGCATAGTTGGCAGCCTCCCTGA  
GGTGCTGCAGGCACCCGTGGGAAGCTCCATTCTGGTGCAGTGCCACTACAGGCTCCAGGA  
TGTCAAAGCTCAGAAGGTGTGGTGCCGGTTCTTGCCGGAGGGGTGCCAGCCCCTGGTGTC  
CTCAGCTGTGGATCGCAGAGCTCCAGCGGGCAGGCGTACGTTTCTCACAGACCTGGGTGG  
GGCCTGCTGCAGGTGGAAATGTTTACCCTGCAGGAAGAGGATGCTGGCGAGTATGGCTG  
CATGGTGGATGGGGCCAGGGGGCCCCAGATTTTGCACAGAGTCTCTCTGAACATACTGCC  
CCCAGAGGAAGAAGAAGAGACCCATAAGATTGGCAGTCTGGCTGAGAACGCATTCTCAGA  
CCCTGCAGGCAGTGCCAACCCTTTGGAACCCAGCCAGGATGAGAAGAGCATCCCCTTGAT  
CTGGGGTGCTGTGCTCCTGGTAGGTCTGCTGGTGGCAGCGGTGGTGCTGTTTGCTGTGAT  
GGCCAAGAGGAAACAAGAATCCCTCCTCAGTGGTCCACCACGTCAGTGACTCTGGACCGG  
CTGCTGAATTGCCTTTGGATGTACCACACATTAGGCTTGACTCACCACCTTCATTTGACA  
ATACCACCTACACCAGCCTACCTCTTGATTCCCCATCAGGAAAACCTTCACTCCCAGCTC  
CATCCTCATTGCCCCCTCTACCTCCTAAGGTCTGGTCTGCTCCAAGCCTGTGACATATG  
CCACAGTAATCTTCCCGGGAGGGAACAAGGGTGGAGGGACCTCGTGTGGGCCAGCCCAGA  
ATCCACCTAACAATCAGACTCCATCCAGCTAAGCTGCTCATCACACTTTAAACTCATGAG  
GACCATCCCTAGGGGTTCTGTGCATCCATCCAGCCAGCTCATGCCCTAGGATCCTTAGGA  
TATCTGAGCAACCAGGGACTTTAAGATCTAATCCAATGTCTAACTTTACTAGGGAAAGT  
GACGCTCAGACATGACTGAGATGTCTTGGGGAAGACCTCCCTGCACCCAACTCCCCCACT  
GGTTCTTCTACCATTACACACTGGGCTAAATAAACCTAATAATGATGTGCAAAAAAAAAA  
AAA

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## FIGURE 282

MGLTLLLLLLLLGLEGGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRFLPEGCQ  
PLVSSAVDRRAPAGRRTFLTDLGGGLLQVEMVTLQEEDAGEYGCMVDGARGPQILHRVSL  
NILPPEEEEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVL  
FAVMAKRKQESLLSGPPRQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 161-181

**N-myristoylation sites:**

amino acids 17-23, 172-178

**Amidation site:**

amino acids 73-79

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## FIGURE 283

GTAGCATAGTGTGCAGTTCACCTGGACCAAAGCTTTGGCTGCACCTCTTCTGGAAAGCTG  
GCCATGGGGCTCTTCATGATCATTGCAATTCTGCTGTTCCAGAAACCCACAGTAACCGAA  
CAACTTAAGAAGTGCTGGAATAACTATGTACAAGGACATTGCAGGAAAATCTGCAGAGTA  
AATGAAGTGCCTGAGGCACTATGTGAAAATGGGAGATACTGTTGCCTCAATATCAAGGAA  
CTGGAAGCATGTAAAAAAATTACAAAGCCACCTCGTCCAAAGCCAGCAACACTTGCCTG  
ACTCTTCAAGACTATGTTACAATAATAGAAAATTTCCCAAGCCTGAAGACACAGTCTACA  
TAAATCAAATACAATTTTCGTTTTCACTTGCTTCTCAACCTAGTCTAATAAACTAAGGTGA  
TGAGATATACATCTTCTTCCTTCTGGTTTCTTGATCCTTAAAATGACCTTCGAGCATATT  
CTAATAAAGTGCATTGCCAGTTAAAAA

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## FIGURE 284

MGLFMIIAILLFQKPTVTEQLKKCWNNYVQGHCRKICRVNEVPEALCENGRYCCLNIKEL  
EACKKITKPPRPKPATLALTLDYVTIIENFPSLKTQST

Important features of the protein:

Signal peptide:

None

Transmembrane domain:

None

cAMP- and cGMP-dependent protein kinase phosphorylation site:

64-68

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## FIGURE 285

GATGGCGCAGCCACAGCTTCTGTGAGATTCTGATTTCTCCCCAGTTCCCCTGTGGGTCTGA  
GGGGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTC  
CCCAAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTTCACTGCAAGTG  
CCTGCTGTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAAT  
AAAGGAGCCACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATC  
TTCTCTTCACGGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCT  
AAGATGAAAGCCTCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGG  
ACTCCTTCCACTGGACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTT  
CAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAAC  
ATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGA  
TGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAG  
ACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATC  
AAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTG  
AAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAA  
AGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAG  
GAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCCACAGTGTA  
TCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCCAATCTTAAT  
TGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATTTATTAG  
TTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATGAAA  
CTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAATAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTG  
TATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACC  
AATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTA  
CAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGG  
AATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAA  
AAAAA



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## FIGURE 287

AATGCCCCATGCGCACCCCCACAGCTCGCGCTCCTGCAAGTGTTCTTTCTGGTGTTCCCCG  
 ATGGCGTCCGGCCTCAGCCCTCTTCCTCCCCATCAGGGGCAGTGCCCCACGTCTTTGGAGC  
 TGCAGCGAGGGACGGATGGCGGAACCCTCCAGTCCCCCTCAGAGGCGACTGCAACTCGCC  
 CGGCCGTGCCTGGACTCCCTACAGTGGTCCCTACTCTCGTGACTCCCTCGGCCCCCTGGGA  
 ATAGGACTGTGGACCTCTTCCCAGTCTTACCGATCTGTGTCTGTGACTTGACTCCTGGAG  
 CCTGCGATATAAATTGCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTT  
 TCTCCTTCTGCCTTCCAGGCAGCGTAAGGTCTTCAAGCTGGGTTTGTGTAGACAACTCTG  
 TTATCTTCAGGAGTAATTCCCCGTTTCTTCAAGAGTTTTCATGGATTCTAATGGAATCA  
 GGCAGTTTTGTGTCCATGTGAACAACTCAAACCTTAACTATTTCCAGAAGCTTCAAAAGG  
 TCAATGCAACCAACTTCCAGGCCCTGGCTGCAGAGTTTGGAGGCGAATCATTCAATCA  
 CATTCCAAACTCAATCACCACCATCTTTTTACAGGGCTGGGGACCCCATTTCTACTTACT  
 TCCCCAAGTGGTCTGTAATAAGCTTGCTGAGACAACCTGCAGGAGTTGGAGCTGGGGGAC  
 TCTGTGCTGAAAGCAATCCTGCAGGTTTCTTAGAGAGTAAAGTACAACCTTGCACTCGTT  
 TTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGATTGAGCCCTCAATGCTGCCTCTTACT  
 ATAACCTTACAGTCTTAAAGGTTCCAAGAAGCATGACTGATCCACAGAATATGGAGTTCC  
 AGGTTCTCTGTAATACTTACCTCACAGGCTAATGCTCCTCTGTTGGCTGGAAACACTTGTC  
 AGAATGTAGTTTCTCAGGTCACCTATGAGATAGAGACCAATGGGACTTTTGGAAATCCAGA  
 AAGTTTCTGTAGTTTGGGACAAACCAACCTGACTGTTGAGCCAGGCGCTTCTTACAGC  
 AACACTTCATCCTTCGCTTCAGGGCTTTTCAACAGAGCACAGCTGCTTCTCTCACCAGTC  
 CTAGAAGTGGGAATCCTGGCTATATAGTTGGGAAGCCACTCTTGGCTCTGACTGATGATA  
 TAAGTTACTCAATGACCCTCTTACAGAGCCAGGGTAATGGAAGTTGCTCTGTAAAAGAC  
 ATGAAGTGCAGTTTGGAGTGAATGCAATATCTGGATGCAAGCTCAGGTTGAAGAAGGCAG  
 ACTGCAGCCACTTGCAGCAGGAGATTTATCAGACTCTTCATGGAAGGCCCAGACCAGAGT  
 ATGTTGCCATCTTTGGTAATGCTGACCCAGCCCAGAAAGGAGGGTGGACCAGGATCCTCA  
 ACAGGCACTGCAGCATTTTCAGCTATAAACTGTACTTCTGCTGTCTCATAACAGTTTCCC  
 TGGAGATCCAGGTATTGTGGGCATATGTAGGTCTCCTGTCCAACCCGCAAGCTCATGTAT  
 CAGGAGTTTCGATTCTTATACCAGTGCCAGTCTATACAGGATTCTCAGCAAGTTACAGAAG  
 TATCTTTGACAACTCTTGTGAACCTTGTGGACATTACCCAGAAGCCACAGCCTCCAAGGG  
 GCCAACCCAAAATGGACTGGAAATGGCCATTCGACTTCTTTCCCTTCAAAGTGGCATTCA  
 GCAGAGGAGTATTCTCTCAAAAATGCTCAGTCTCTCCCATCCTTATCCTGTGCCTCTTAC  
 TACTTGGAGTTCTCAACCTAGAGACTATGTGAAGAAAAGAAAATAATCAGATTTTCAGTTT  
 TCCCTATGAGAACTCTGAGGCAGCCACTTATCTTGGCTAAATAGAACCTCACCTGCTCA  
 TGACCAGAGAGCATTTAGGATAATAGATGACCTAACTGAAGGAATCCTTGTATATGAAAG  
 GAGTTATTTTAGAAAAGCAATAAAAATATTTTATTTCATCNTAAAAA

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## FIGURE 288

M RTPQLALLQVFFLVFPDGV RPQPSSSPSGAVPTSLELQRGTDGGTLQSPSEATATRP  
PGLPTVVPTLVTPSAPGNRTVDLFPVLPICVCDLTPGACDINCCCDRDCYLLHPRTVFSF  
CLPGSVRSSSWVCVDNSVIFRSNSPFPSRVFMD SNGIRQFCVHVNN SNLNYFQKLQKVNA  
TNFQALAAEFGGESFTSTFQTQSPPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCA  
ESNPAGFLESKSTTCTRFFKNLASSCTLDSALNAASYNFTVLKVPRSM TDPQNMEFQVP  
VILTSQANAPLLAGNTCQNVVSQVTYE IETNGTFTGIQKVS VSLGQTNLTVEPGASLQQHF  
ILRFRAFQQSTAASLTSPRSGNPGYIVGKPLLALTDDISYSMTLLQSQNGSCSVKRHEV  
QFGVNAISGCKLRLKKADCSHLQQEIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRH  
CSISAINCTSCCLIPVSLEIQVLWAYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSL  
TTLVNFVDITQKPQPPRGQPKMDWKWPFDFFPFKVAFSRGVFSQKCSVSPILILCLLLLG  
VLNLETM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 484-505, 581-600

**N-glycosylation sites:**

amino acids 78-82, 165-169, 179-185, 279-285, 331-337,  
347-351, 410-414, 487-491

**N-myristoylation sites:**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 420-431



# FIGURE 289

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACC  
 CCGCGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCTGAGCCTCGGGCTCCGGCCC  
 GGACCTGCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAG  
 AAAGATGGCTTTAAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATT  
 ACTAGGCTATTTGTTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATT  
 CAGGGATCGGTCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTC  
 TAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAG  
 GTTCAAGGAGGACTGGGGCTTCAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAA  
 CCGCTTTCAGAAGGCAAATTGTTTCAGCCACCAGTGATGCCATCTGCCGGGACTGCTTGCC  
 AGGATTTTATAGGAAGACGAACTTGTGCGCTTTCAGACATGGAGTGTGTGCCTTGTGG  
 AGACCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGC  
 GTCCACGGCCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGC  
 CACCGTCCTGCTGGCCCTGCTCATCCTCTGTGTCTATCTATTGTAAGAGACAGTTTATGGA  
 GAAGAAACCCAGCTGGTCTCTGCGGTGCGCAGGACATTCAGTACAACGGCTCTGAGCTGTC  
 GTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCCTGCTGCCAGTGCCGCCG  
 TGACTCAGTGCAGACCTGCGGGCCGGTGCCTTGCTCCCATCCATGTGCTGTGAGGAGGC  
 CTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCCAGTCTTCAGGC  
 AAGAAACGCAAGCCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTCACGCAGTC  
 CATCTGTGGCGAGTTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGTGACAA  
 CATCTCTTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAATCC  
 AGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGC  
 TGTTCCAGTCCAGTCTCATTCTGAAAACCTTACAGCAGCTACTGATTTATCTAGATATAA  
 CAACACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGA  
 TCAGGAGAGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAG  
 AACCTGCTTCTTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTAG  
 GCTTATGGACTGAGCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATAAATCTGAACC  
 AAAGTACGGCATTGTAAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCT  
 GAAACCTCAATGAATAACAAGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTC  
 CTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCA  
 GCCTATGAGATTGTGGACATATAACAAGAAACAGAAATGCCCTCATGCTTATTTTCATGG  
 TGATTGTGGTTTTTACAAGACTGAAGACCCAGAGTATACTTTTTCTTTCAGAAATAATTT  
 CATAACCGCCTATGAAATATCAGATAAATTACCTTAGCTTTTATGTAGAATGGGTTCAAAA  
 GTGAGTGTTTCTATTTGAGAAGGACACTTTTTTCATCATCTAAACTGATTTCGCATAGGTGG  
 TTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTTTATTAGATGAAGTTTACTGAA  
 TCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCCACACTTCTGACCTCAGCC  
 TCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTAGGGAATGTGGTCGAG  
 AAAGGGCAGCCCATGCCCAGAAATTAACACATATTGTAGAGACTTGTATGCAAAGGTTGG  
 CATATTTATATGAAAATTAGTTGCTATAGAAAACATTTGTGTGCATCTGTCCCTCTGCCTGA  
 GCTTAGAAGGTTATAGAAAAGGGTATTTATAAACATAAATGACCTTTTACTTGCATTGT  
 ATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCCTACTACTGAAGTAGC  
 CTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT  
 GGATGAAGCAGCTGTAAGTGCCTAGTGTAGTTTGACCAGGACATTTGTCGTGCTCCTTCC  
 AATTGTGTAAGATTAGTTAGCACATCATCTCCTACTTTAGCCATCCGGTGTGGATTAA  
 GAGGACGGTGCTTCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTG  
 TCTCTAGAGCTAAGACAGAAATTAACCCCGTTTCAGTCACAAAGCAGGGAATGGTTTCAATTT  
 ACTCTTAATCTTTATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTAGACTTC  
 TGAACATCAGTATGTTTCGAGGGTACTATGATATTTTGGTTTGGAAATTGCCCTGCCCAAGT  
 CACTGTCTTTTAACTTTTAACTGAATATTAAAATGTATCTGTCTTTCCT

## FIGURE 290

MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK  
 ECGFGYGEDAQCVTCLHRFKEDWGFQKCKPCLDCAVVNRFOKANCSATSDAICGDCLPG  
 FYRKTCLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT  
 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRD  
 SVQTCGPVRLLPSCMCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI  
 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV  
 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA

### Important features of the protein:

#### Signal peptide:

Amino acids 1-25

#### Transmembrane domain:

Amino acids 169-192

#### N-glycosylation sites:

Amino acids 105-109; 214-218; 319-323; 350-354; 368-372; 379-383

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204; 238-242

#### Tyrosine kinase phosphorylation site:

Amino acids 207-214

#### N-myristoylation sites:

Amino acids 55-61; 215-221; 270-276

#### Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

#### TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

CCTGGAGCCGGAAGCGGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTTCGGTTCCGCATC  
CAGCCTAGTCGTGTCCACGATGCGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCG  
ATCGAGGTGCTTAGGGATCGCGGTCTTTCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCC  
TCTGCCAGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCTCGGCTGGAGCCAGT  
TCTAACTGGACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGAT  
GCCTTGAGAGATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACA  
TACCTTGTGAAAAAGGAGCATCTCACAGTTTTTGTGGCTGAAGCAAAGCCACCTACAGTT  
ACTATGCCTCGAATCAAGGCATTGATGACGGGGAGCCTTTCCTGGCTTTGTTCGACGTCATC  
AGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCT  
GAAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTAATCCCAAAGCATTTT  
GTGGAATATGATGGAACAACCTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAAT  
GTCACGAGGCATTTGGATAAAGTATTA AAAAGAGGAGATTGGGACATATTAATCCTCCAC  
TACCTGGGGCTGGACCACATTGGCCACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAG  
AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTACTGCAGTCGAAGGAG  
AGAGAGACGCCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACA  
GGAAGTCACGGGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCT  
GCGTTTGAAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTG  
GCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTC  
CTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTTTACATTTGAAT  
ACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTCATATGAAAAAGATCCTGGG  
TTTGAGCAGTTTAAATGTGAGAAAGATTGCATGGGAACTGGATCAGACTGTACTTGGAG  
GAAAAGCATTACAGAAGTCCTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGAT  
GCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCAGTTCTCACCCCTGCTCC  
TGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTCATCTC  
CTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCGTTACAGTCATTG  
TGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT  
GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGGCAGTGCCC  
TGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGTGTCCC  
GACACAGGTGTTACATCTGTGCTGTCAGGTGAGATGCCTCAGTTCTTGGAAAGCTAGGT  
TCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCC  
CAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCACAGAGGTGTGGGAGCTGCAGCTGA  
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTGCACAC  
ACTCATCCTGCCACCCCAAGATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGG  
CGGACGTTTTCTGTTGGAATCTTAGTCCTTGGCCTCGGACACCTTCATTTCGTTAGCTGG  
GGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACTCAGATCCACAGAGCCCCA  
GGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCCAACCTGCAC  
AGCCCTCATCCCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGA  
CACTCACAGCTTTGTCTATCAGGGCACAGGCTTCTTCGGAGCCAGGATGATCTGTGCCACG  
CTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTTACCAAAAAGATAAACGGCAATAATTGAGAAAAAAA

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## FIGURE 292

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL  
PPPLFSKVIVLIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIK  
ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGT  
TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHISGPNSPLIGQKLSEMD  
SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP  
GDIRHPKHVQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites:**

amino acids 56-60, 194-198

**N-myristoylation sites:**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site:**

amino acids 154-158

**Cell attachment sequence:**

amino acids 205-208

## FIGURE 293

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCA  
 ATGGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGG  
 TCCCAAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGG  
 GCCATGAAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTG  
 GACACCGGGTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCT  
 GCGGGCCAGACGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGC  
 TGCACAACTGACAAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGC  
 CAAGCACCCGACCCGCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCAC  
 CAGGATGACTGCGCTATCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCC  
 TGCTTCCAGGGCAGTGGCAGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGA  
 ACCTGCCACCGGCCCTCCTGCACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGAC  
 CTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTC  
 ACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCA  
 GTCCTCCTGCTGGTGGGGCTCTCAGCATAGACCGCCCCTCCAGGATGCTGGGGACAGGGC  
 TCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGCTCACTGGAAAATGATGTT  
 AAAGTAAGAATTGCAAAA

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## FIGURE 294

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAIL  
SLDTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPN  
LSQAPDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVY  
IRTCHRPSCCTTEGTTSPWTAIDLQSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALL  
LPVLLLVLGLSA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 233-251

**N-glycosylation sites:**

amino acids 120-124, 174-178

**N-myristoylation sites:**

amino acids 15-21, 84-90

## FIGURE 295

AATCGGCTGATTCTGCATCTGGAACTGCCTTCATCTTGAAAGAAAAGCTCCAGGTCCCT  
TCTCCAGCCACCCAGCCCCAAGATGGTGATGCTGCTGCTGCTGCTTTCCGCACTGGCTGG  
CCTCTTCGGTGCGGCAGAGGGACAAGCATTTTCATCTTGGGAAGTGCCCCAATCCTCCGGT  
GCAGGAGAATTTTGACGTGAATAAGTATCTCGGAAGATGGTACGAAATTGAGAAGATCCC  
AACAACCTTTGAGAATGGACGCTGCATCCAGGCCAACTACTCACTAATGGAAAACGGAAA  
GATCAAAGTGTTAAACCAGGAGTTGAGAGCTGATGGAAGTGTGAATCAAATCGAAGGTGA  
AGCCACCCCAGTTAACCTCACAGAGCCTGCCAAGCTGGAAGTTAAGTTTTCCTGGTTTAT  
GCCATCGGCACCGTACTGGATCCTGGCCACCGACTATGAGAACTATGCCCTCGTGTATTC  
CTGTACCTGCATCATCCAACCTTTTTCACGTGGATTTTGCTTGGATCTTGGCAAGAAACCC  
TAATCTCCCTCCAGAAACAGTGGACTCTCTAAAAAATATCCTGACTTCTAATAACATTGA  
TGTCAAGAAAATGACGGTCACAGACCAGGTGAACTGCCCCAAGCTCTCGTAAACAGGTTC  
TACAGGGAGGCTGCACCCACTCCATGTTACTTCTGCTTCGCTTTCCCCTACCCACCCCC  
CCCCCATAAAGACAAACCAATCAACCACGACAAAGGAAGTTGACCTGAACATGTAACCAT  
GCCCTACCCTGTTACCTTGCTAGCTGCAAAATAAACTTGTTGCTGACCTGCTGTGCTCGC  
AAAAAA

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## FIGURE 296

MVMLLLLLLSALAGLFGAAEGQAFHLGKCPNPPVQENFDVNKYLGRWYEIEKIPTTFENG  
RCIQANYSLMENGKIKVLNQELRADGTVNQIEGEATPVNLTETPAKLEVKFSWFMPSAPY  
WILATDYENYALVYSCTCIIQLFHVDFAWILARNPNLPPETVDSLKNILTSNNIDVKKM  
TVTDQVNCPKLS

**Signal sequence:**

1-16

**N-glycosylation site:**

65-68

98-101

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

175-178

**N-myristoylation site:**

13-18

16-21

**Lipocalin proteins:**

36-47

120-130

**Lipocalin / cytosolic fatty-acid binding proteins:**

41-185



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## FIGURE 297

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGC  
TGCCTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATA  
GTGGGCGTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCA  
AGGTAATTCAGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATG  
CAGCACCAAAAAAGGACTCACCTCCCAAAAATTCGCTGAAGGTTGATGAGCTTTCACCTCT  
ACTCAGTTCCTGAGGGTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAA  
GCATCTCACAGCTCCGACACTATTGCGAGCCATACACAACCTGGTGTGAGGAAACGTACT  
CCCAAATAAGCCCAAGATGCAAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATC  
TCCAAAATGCACCTCCTGGATTTTTTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTA  
TTGGACTCCTTTTGGCTAGAGGTTCAAAAATAAAGAAGCTAGTGTATCCGCCTGGTTTTCA  
TGGGATTAGCTGCCTCCCTCTATTATCCACAACAAGCCATCGTGTTTTGCCCAGGTCAGTG  
GGGAGAGATTATATGACTGGGGTTTACGAGGATATATAGTCATAGAAGATTTGTGGAAGG  
AGAACTTTCAAAGCCAGGAAATGTGAAGAATTCACCTGGAATAAGTAGAAAACTCCAT  
GCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAACTCCATAGAATAAATCAGTAT  
TTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTAAATTGGCTTTCTTCTTCA  
GGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCTACAAGCAAATAACC  
TGGAATCCCTTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCATTTCTCATGTTGCT  
ATTTATGTACCTAATTAAAACCCAAGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAA

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## FIGURE 298

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEESISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLLLARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPGNVKNSPGTK

**Important features:**

**Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 111-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 36-44

**N-myristoylation sites:**

Amino acids 124-130;144-150;189-195

## FIGURE 299

CCGCTGAGATGTACGAACTTCCGGTTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCA  
 CCTGCCACGACCGGGCCTCTCCCTGGCGTTTGGTCACCTCTGCTTCATTCTCCACCGCGC  
 CTATGGTCCCTCTTGGAGCCAGCGTGGCGGGCCTGGCGGCTCCCGGGTGGTGAGAGAGCG  
 GTCCGGGAACGATGAAGGCCTCGCAGTGCTGCTGCTGTCTCAGCCACCTCTTGGCTTCCG  
 TCCTCCTCCTGCTGTTGCTGCCTGAACTAAGCGGGCCCCTGGCAGTCCTGCTGCAGGCAG  
 CCGAGGCCGCGCCAGGTCTTGGGCCTCCTGACCCTAGACCACGGACATTACCGCCGCTGC  
 CACCGGGCCCTACCCCTGCCAGCAGCCGGGCGGTGGTCTGGCTGAAGCTGCGGGGCCG  
 GGGGCTCCGAGGGAGGCAATGGCAGCAACCCTGTGGCCGGGCTTGAGACGGACGATCACG  
 GAGGGAAGGCCGGGGAAGGCTCGGTGGGTGGCGGCCTTGCTGTGAGCCCCAACCCCTGGCG  
 ACAAGCCCATGACCCAGCGGGCCCTGACCGTGTGATGGTGGTGAGCGGCGCGGTGCTGG  
 TGTACTTCGTGGTCAGGACGGTCAGGATGAGAAGAAGAAACCGAAAGACTAGGAGATATG  
 GAGTTTTTGACACTAACATAGAAAATATGGAATTGACACCTTTAGAACAGGATGATGAGG  
 ATGATGACAACACGTTGTTTGATGCCAATCATCCTCGAAGATTAAGAATGTGCCTTTTGAT  
 GAAAGAACTTTATCTTTCTACAATGAAGAGTGGAATTTCTATGTTTAAAGGAATAAGAAGC  
 CACTATATCAATGTTGGGGGGGTATTTAAGTTACATATATTTTAAACAACCTTTAATTTGC  
 TGTTGCAATAAATACCGTATCCTTTTATTATATCTTTATATGTATAGAAGTACTCTATTA  
 ATGGGCTCAGAGATGTTGGGGATAAAGTATACTGTAATAATTTATCTGTTTGAAAATTAC  
 TATAAAACGGTGTTTTCTGGTCGGTTTTTGTTCCTGCTTACCATATGATTGTAAATTGT  
 TTTATGTATTAATCAGTTAATGCTAATTATTTTTGCTGATGTCATATGTAAAGAGCTAT  
 AAATTTCCAACAACCAACTGGTGTGTAAAAATAATTTAAAATTTCTTTACTGAAAGGTAT  
 TTCCCATTTTTGTGGGGAAAAGAAGCCAAATTTATTACTTTGTGTTGGGGTTTTTAAAT  
 ATTAAGAAATGTCTAAGTTATTGTTTGCAAAACAATAAATATGATTTTAAATTCTCTTAA  
 AAAAAAA

## FIGURE 300

MKASQCCCCLSHLLASVLLLLLLPELSGPLAVLLQAEEAAPGLGPPDPRPRTLPPPLPPGP  
TPAQQPGRGLAEAAAGPRGSEGGNGSNPVAGLETDDHGGKAGEGSVGGGLAVSPNPGDKPM  
TQRALTVLMVVS GAVLVYFVVRTVRMRRNRKTRRYGVLD TN IENMELTPLEQDDEDDDN  
TLFDANHPRR

**Signal peptide:**  
amino acids 1-28

**Transmembrane domain:**  
amino acids 124-140

**N-glycosylation site:**  
amino acids 83-87

**N-myristoylation sites:**  
amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,  
157-160

# FIGURE 301

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTT  
 CCCGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCAATGGGACCTGTGC  
 GGTTGGGAATATTGCTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGA  
 AGGAGGAGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGA  
 GCACAGAGCTACAGGCGGAAGTGCACACCGGTCGATCTCGAGAGGTGCTGGAGCTGG  
 GGCAGGTGCTGGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAA  
 GGCTGGAAGAGGCCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACAGCTG  
 AGCGCAAGGGCTCACTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAG  
 GCCTAGTGCAGAAGGGGGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGC  
 CCAGCGTGGAGGTCACATACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAG  
 ACATTGTGGGAGACTGGTACTTCCACCATCAGGAGCAGCCCCTACAAAATTTTCTCTGTG  
 AAGGTCATGTGCTCCCAGCTGCTGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGG  
 AGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAG  
 AGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAGGAAGCCACCCCAAACCTTGACC  
 GAGAAGATCTTTTGACCCTTGCCCTTTGAGCCCCCAGGAGGGGAAGGGATCATGGAGAGCCC  
 TCTAAAGCCTGCACCTCTCCCTGCTCCACAGCTTTTCAGGGTGTGTTTATGAGTGACTCCAC  
 CCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGGTGAAACAGCATG  
 ACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCCTGCTCCTAGAGATGAACTCTATC  
 CAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTTAACTGA  
 TCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTCACT  
 TAGCTCCTTAAGGTCTGTTTTTTAGACCCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT  
 GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAA  
 TGGGACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCT  
 ACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTTCTAT  
 ATCGCTATTAACTTTTTTCTTTTTTTCTA

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## FIGURE 302

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSR TGRSRE  
VLELGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTM  
ATLKGLVQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQ  
NFLCEGHVLPAAETACLQETWTGKEITDGEKTEGEEEEEEEEEEEEEGGDKMTKTGSH  
PKLDREDL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 106-110

**N-myristoylation site:**

amino acids 115-121

**Amidation site:**

amino acids 70-74

# FIGURE 303

CTCCTGCACTAGGCTCTCAGCCAGGGATGATGCGCTGCTGCCGCCGCCGCTGCTGCTGCC  
GGCAACCACCCCATGCCCTGAGGCCGTTGCTGTTGCTGCCCCCTCGTCCTTTTACCTCCCC  
TGGCAGCAGCTGCAGCGGGCCCAAACCGATGTGACACCATATAACCAGGGCTTCGCCGAGT  
GTCTCATCCGCTTGGGGGACAGCATGGGCCGCGGAGGCGAGCTGGAGACCATCTGCAGGT  
CTTGGAATGACTTCCATGCCTGTGCCTCTCAGGTCCTGTCAGGCTGTCCGGAGGAGGCAG  
CTGCAGTGTGGGAATCACTACAGCAAGAAGCTCGCCAGGCCCCCCCGTCCGAATAACTTGC  
AACTCTGTGCGGTGCCCCGGTGCATGTTTCGGGAGCGCGGCACAGGCTCCGAAACCAACC  
AGGAGACGCTGCGGGCTACAGCGCCTGCACTCCCCATGGCCCCCTGCGCCCCCACTGCTGG  
CGGCTGCTCTGGCTCTGGCCTACCTCCTGAGGCCTCTGGCCTTAGCTTGTTGGGTTGGGTA  
GCAGCGCCCGTACCTCCAGCCCTGCTCTGGCGGTGGTTGTCCAGGCTCTGCAGAGCGCAG  
CAGGGCTTTTCATTAAAGTATTTATATTTGTA

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## FIGURE 304

MMRCCRRRCCCRQPPHALRPLLLLPLVLLPPLAAAAAGPNRCDTIYQGFAECLIRLGDSM  
GRGGELETICRSWNDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGAPVH  
VRERGTGSETNQETLRATAPALPMAPAPPLLAALALAYLLRPLA

**Signal peptide:**

Amino acids 1-35

**Transmembrane domain:**

Amino acids 141-157

**N-myristoylation site:**

Amino acids 127-133

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 77-88



## FIGURE 305

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCC  
 TTCTCCCTGTGCTTAACCAGAGGTGCCCATGGGTTGGACAATGAGGCTGGTCACAGCAGC  
 ACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGC  
 CCATGAGGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCC  
 AGAGTTGGGGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACCTACAGACAGAAGAT  
 CACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATAT  
 CCTGGTGATGGTGGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAG  
 ACATTGGCTGGTAACAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCA  
 GGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCA  
 GTTCTTTGTCTATCTTCAGGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAAC  
 TCGAGGCTCTTGGAATGGACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGC  
 AAGCACCAGTTTCATGACCCAGAACTACCAGGACTACCAACCCTCCAGGCTCCAGAGG  
 AAGGGCCAGCGAGCCCAAGCACAAAACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGC  
 TTTGCCATCCGGGCATGTGGCCACACTGCTCACCACCGACGATGTGGGTATGGAACCCCC  
 TCTGGATACAGAACCCTTCTTTTCCAAATTAAAAAATAATCATCAA

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## FIGURE 306

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV  
VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG  
ADLKKGKIQQQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRF  
LNRFHLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site:**

amino acids 169-173

**Tyrosine kinase phosphorylation site:**

amino acids 59-68

**N-myristoylation sites:**

amino acids 54-60, 83-89, 130-136

**Phosphatidylethanolamine signature:**

amino acids 113-157

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## FIGURE 307

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGC  
 TCCTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGA  
 TTTCCACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAG  
 CTAAGGACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATT  
 AGCCCTTAGATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGT  
 TCAAGGATCATCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACT  
 CTTTCTCTACATGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCA  
 GGCAGGAAGCCACCAATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCC  
 ACGCTGCTGCCATTAAATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGA  
 ATCATGAAGTAATGTTCTCAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAA  
 CACCCCCTGTGCGGTTTACTGTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAA  
 GGCCCCTTGCAGCTGAAAGTCCCCTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAA  
 TAGGCAAAAAGTCTACTGTGGTATTTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGG  
 CCATCCTGGGAGTAAAGGGCTGCCTTCCCATCTAATTTATTGTAAAGTCATATAGTCCAT  
 GTCTGTGATGTGAGCCAAGTGATATCCTGTAGTACACATTGTACTGAGTGGTTTTTCTGA  
 ATAAATTCATATTTTACCTATGA

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## FIGURE 308

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTIL  
STLETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQ  
CQEQRQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites:**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 102-106

**N-myristoylation site:**

amino acids 24-30

**Actinin-type actin-binding domain signature 1:**

amino acids 159-169

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## FIGURE 309

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCAGTCCCCTGGACTGTAGATAAA  
GACCCTTTCTTGCCAGGTGCTGAGACAACCACACTATGAGAGGCACTCCAGGAGACGCTG  
ATGGTGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATC  
CAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTATTTGGGAATCCAGAATCCAGAAA  
TGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGA  
TCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGA  
CTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCA  
AGAGAGACCAGCCCATCATTCCTGACTTCAGAACTTGGAAGTCATACAACACTGCCTTTG  
AATTAAATATAAATGACTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGT  
TTCTGGTTCCTCAATGTGTTTTTCGTCTACATTTTCTTAGTGTCATTTTCACGCTGGTGCTG  
AGACAGGAGCAAGGCTGCTGTTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTC  
ATAGCAACTGAAGAACAGGATGTGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTG  
TCCTCTCAAGCTGGTGCTGTGTAGGCCACAAGGCATCTGCATGAGTGACTTTAAGACTCA  
AAGACCAAACACTGAGCTTTCTTCTAGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCG  
CGTTACCCACGATGGCATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTC  
CCTCTTGGGATGATATCATCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAAT  
AGAACCTTCTTAGCATTAAAGACCTTGTAACAAAAATAATTCTTGGGGTGGGTATGAAGA  
TGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACAGAGCTGATCTCTGT  
TTCTGTTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTATATGTTGCCAATA  
TACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAGACCTTGTAACAAAAATAATTCT  
TTGTGTTAAGTTAAATCATTTTTGTCTTAATTGTAATGTGTAATCTTAAAGTTAAATAAA  
CTTTGTGTATTTATATAATAATAAAGCTAAAACCTGATATAAAAATAAAGAAAGAGTAAACTG

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## FIGURE 310

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQP  
TLQLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSEL  
GKSYNTAFELNIND

**Signal sequence:**

amino acids 1-17

**N-myristoylation site:**

amino acids 10-16

**Cell attachment sequence:**

amino acids 36-39

# FIGURE 311

GCGAGGCTGCACCAGCGCCTGGCACC**AT**GAGGACGCCTGGGCCTCTGCCCCGTGCTGCTGC  
TGCTCCTGGCGGGAGCCCCGCGCGCGGCCCACTCCCCGACCTGCTACTCCCGCATGC  
GGGCCCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGG  
AGCCATGTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGG  
ACAAGCTGCGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCT  
TGAAGGACAAAGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGG  
TATTCCTGTTGGATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGC  
CAGATCGTCAGCGCT**TA**AGGGAAGTGAAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTAT  
GTCAGCTACCCAGACTTAATGGGCCAGAGCCATGACCCCTCACAGGTCTTGTGTTAGTTGT  
ATCTGAAACTGTTATGTATCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAG  
GAACCTCCTTTGAGCATAGAGTTAGCAACCATGCTTCTCATTCCCTTGACTCATGTCTTG  
CCAGGATGGTTAGATACACAGCATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAAC  
AAGCTTCACTTTTATGAACAACATATTTTGAGAACATGCACAATAGTATGTTTTTATTACT  
GGTTAATGGAGTAATGGTACTTTTATTCTTTCTTGATAGAAACCTGCTTACATTTAACC  
AAGCTTCTATTATGCCTTTTCTAACACAGACTTTCTTCACTGTCTTTTCAATTTAAAAAGA  
AATTAATGCTCTTAAGATATATATTTTACGTAGTGCTGACAGGACCCACTCTTTCATTGA  
AAGGTGATGAAAATCAAATAAAGAATCTCTTCACATGGA

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## FIGURE 312

MRTPGPLPVLLLLLAGAPAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPR  
LYLDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNA  
LEYPIPVTTVLPDRQR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 60-69

**N-myristoylation site:**

amino acids 16-22



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## FIGURE 313

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCT  
AATCTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCAT  
CAAAGCTTTGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCAT  
CCAGGTGAAAGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAA  
CCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGTTGA  
CAATCAGTTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGT  
TGAAGATATATCCGAAACCAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGT  
TCCTCCAAGGATAAAATCAAGAACGAACCAAATTTAAAATCACATTCAAGTCCGATGACTA  
CTTTGTGGCTAAACCTGGATTCAAGATTTATTATTCTTTGCTGGAAGATTTCCAACCCGC  
AGCAGCTTCAGAGACCAACTGGGAATCTGTCACAAGCTCTATTTCAAGGGGTATCCTATAA  
CTCTCCATCAGTAACGGATCCCACTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAGA  
ATTTGATACAGTGGAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAGATCT  
TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTCATACCATGACCGGAAGTC  
AAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTTGCACTCCAGGAA  
TTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGTGGTCTTCTTTCCACGTTG  
CCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAACCTGTCAACTGGAGGTCCTG  
CACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGTATTACAGTTTGAGCCTGG  
CCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGATCA  
CCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATTAAGAGAATGTGCACAT  
CCTTACATTAAGCCTGAGAGAA

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## FIGURE 314

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKGNQYVQS  
PRFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEEAENDICRYDFVEVEDISETSTII  
RGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESV  
TSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRY  
RGRSYHDRKSKVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGGNC  
GCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSS  
RPPR

**Signal peptide:**

amino acids 1-18

**N-glycosylation site:**

amino acids 270-274

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 262-266

**Tyrosine kinase phosphorylation site:**

amino acids 256-265

**N-myristoylation sites:**

amino acids 94-100, 186-192, 297-303, 298-304

**TonB-dependent receptor proteins signature 1:**

amino acids 1-56

## FIGURE 315

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAG  
CTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTG  
CTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTA  
GGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATC  
CTGGGTGTCCAGGGTGGAAAGCCAGTGCCTGTCTATGTGGGGTGGGGCAGGAGCCGACTCTA  
ACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTC  
ACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCTTCGAGTCGGCTGCCTACCCGGGC  
TGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTGTGAGCTCACCCAGCTTCCCGAG  
AATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAAC  
GTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCC  
ATGGCGGACAATCACTCTCTGCTCTCAGGACCCCCACGTCTGACTTAGTGGGCACCTG  
ACCACTTTGTCTTCTGGTTCAGTTTGGATAAATTCTGAGATTGAGGCTCAGTCCACG  
GTCCTCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTAAGAACCATGTGGGGTAA  
CTGGGAATAACATGAAAAGATTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTC  
CTGCTTAATGGTAAGTGAACAAGTGTACCTGAGCCCCGAGGCCAACCCATCCCCAGTT  
GAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTCCTGTCACTCACCAGTGTGAGGAG  
AGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCTTGCCCGAGCCCCACCCCTCCCT  
TTAATCCTGCCACTGTCTATGCTACCTTTCTCTATCTCTTCCCTCATCTCTTGTGTGG  
GCATGAGGAGGTGGTGTGATGTGTCAGAAAGAAATGGCTCGAGCTCAGAAGATAAGATA  
GGGTATGCTGATCCTCTTTTAAAGAACCAAGATACAATCAAAATCCCAGATGCTGGTCTC  
TATTCCCATGAAAAGTGCTCATGACATATTGAGAAGACCTACTTACAAAGTGGCATATA  
TTGCAATTTATTTTAAATTAAGATAACCTATTTATATATTTCTTTATAGAAAAAGTCTG  
GAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTATAGGTGATTTTCTTT  
TAATTCTGTTAATTTATCTGTATTTCTTAATTTTCTACAATGAAGATGAATTCCTTGTA  
TAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGATTGTC  
CTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG  
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAG  
TTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAAAGAACAAAAATCATCTGGTAATTCT  
TTCCTAGAAGGATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGC  
TGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAATCTCAGTCTG  
TGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGG  
ATGAAGGTAGACCTAAATTCAATATGACTGGTTTCCTTGTATGAAAAGGAGAGGACACAG  
AGACAGAGGAGACGCGGGGAAGACTATGTAAAGATGAAGGCAGAGATCGGAGTTTTCAG  
CCACAAGCTAAGAAACACCAAGGATTGTGGCAACCATCAGAAGCTTGGAAGAGGCAAGA  
AGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTGCTGAAACCTTAATCTCAGAC  
TTCCAGCCTCCTGAACGAAGAAAGATAAATTTTCGGCTGTTTTAAGCCACCAAGGATAAT  
TGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGTCTCCTCGTGT  
TTACATTCTGTGTGTGTCCCCCTCCCACAATGTACCAAGTTGTCTTTGTGACCAATAGAA  
TATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAGAGACTGCAGCTTC  
TACTTGAGCCCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCT  
GGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCTATAAGAGACTTACGTGGTAAAAAAT  
GAAGTCTCCTGCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATC  
GATGTTTGTGTTGTTTAAAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAA  
TAATATGCAGAGAAAGAG

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## FIGURE 316

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILG  
VQGGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF  
LCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD

**N-myristoylation sites:**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature:**

amino acids 111-131

**Interleukin-1 proteins:**

amino acids 8-29, 83-120, 95-134, 64-103

## FIGURE 317

ATGGAACTTGGACTTGGAGGCCTCTCCACGCTGTCCCACTGCCCCCTGGCCTAGGCGGCAG  
CCTGCCCCTGTGGCCACCCCTGGCCGCTCTGGCTCTGCTGAGCAGCGTCGCAGAGGCCTCC  
CTGGGCTCCGCGCCCCGCAGCCCTGCCCCCGCGAAGGCCCCCGCCTGTCCTGGCGTCC  
CCCGCCGGCCACCTGCCGGGGGGACGCACGGCCCGCTGGTGCAGTGGAAGAGCCCGGCGG  
CCGCCGCCGCAGCCTTCTCGGCCCCGCGCCCCCGCCGCCTGCACCCCCATCTGCTCTTCCC  
CGCGGGGGCCGCGCGGCGCGGGCTGGGGGCCCCGGGCAGCCGCGCTCGGGCAGCGGGGGCG  
CGGGGCTGCCGCCTGCGCTCGCAGCTGGTGCCGGTGCGCGCGCTCGGCCTGGGCCACCGC  
TCCGACGAGCTGGTGCGTTTCCGCTTCTGCAGCGGCTCCTGCCGCCGCGCGCGCTCTCCA  
CACGACCTCAGCCTGGCCAGCCTACTGGGCGCCGGGGCCCTGCGACCGCCCCCGGGCTCC  
CGGCCCCGTCAGCCAGCCCTGCTGCCGACCCACGCGCTACGAAGCGGTCTCCTTCATGGAC  
GTCAACAGCACCTGGAGAACCGTGGACCGCCTCTCCGCCACCGCCTGCGGCTGCCTGGGC  
TGA

## FIGURE 318

MELGLGGLSTLSHCPWPRRQPALWPTLAALALLSSVAEASLGSAPRSPAPREGPPPVLAS  
PAGHLPGGRTARWCSEGRARRPPPQPSRPAPPPPAPPSALPRGGRAARAGGPGRARAAGA  
RGCRLRSQLVFVRALGLGHRSEDLVRFRFCSGSCRRARSPHDLSLASLLGAGALRPPPGS  
RPVSQPCCRPTRYEAVSFMDVNSTWRTVDRLSATAACGLG

**signal sequence:**

Amino acids 1-39

**N-glycosylation site:**

Amino acids 202-206

**N-myristoylation sites:**

Amino acids 6-12;67-73;102-108;109-115;119-125

## FIGURE 319

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCAC  
 AGACGTGAGCCACTCCACCCAGCCTAAAACCTTCATCTTCTTTGGATGAGATGAACACTTT  
 TAACAAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCA  
 CTGACTGAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAAA  
 CTTACACAGTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGT  
 AGAGCCAGATCGTCATCATGTCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGG  
 ACTTGTCTGAAAGCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTG  
 GAGCATCTTGTGGGATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTTCGTGCTTCTG  
 AAAGGCTGGCTGAAATAGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCA  
 TTGGCCAAAAGTACTGCATGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTC  
 CCGGTGACAAAATTCTGGTCAACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCT  
 CTCAAGCTCCCACATCCTGGATTAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGA  
 CTACTAGAATCAAAGAAATCCAGAGGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGA  
 GAGGTGGACTCTGTGCCTACAGTGGGGGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGA  
 GCTGTGACTTCTGCAATGATGTCCTTGCACGAGCCAAGTACCTCAAGAGACATGGCTTCT  
AACATCTCAGATGAAACCCAAGACCATGATCACATATGCAGCCTCAAATGTTACACAGAT  
 AAACTAGCCAAGGGCACCTGTAACTGGGAATCTGAGTTTGACCTAAAAGTCATTAAAAT  
 AACATGAATCCCATTAATAAAAAAAAAAAAAA

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## FIGURE 320

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEI  
DMPYLLKYQPMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTS  
WISESQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCN  
DVLARAKYLKRHGF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

**Amidation site:**

amino acids 40-44



## FIGURE 321

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCCTGGGGCT  
GAGAGTTCACCTGTCTCAGGAACACCTGAGCCCACAGATCCTGTGGGCAGCGGCCAGGG  
CAGCCATGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTCC  
GTGCCTCCACGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTG  
AAATTGGGAAAGCCCCCTCTCCAGCGGGCCCTGCAGGTCACCTGTCCCTCATTTCCCTGGACT  
GGAGTGGAGAGGCGCTTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCC  
TCCACCTGAAATTCAATTGCTGGTTTCGGAGTGCGCCTGCTGGCAGCAGCTAATTTTACTT  
TCAAGGTCTTTTCGCGCCCCAGAGCCCCCTGGAGCTGACGCTGCCTGTGGAACCTGCTGGCTG  
ACACCCGCGTGACCCAGAGCTCCATCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTT  
TATTTCTCGGGCCACGCCAACGAGTTTGATGGCAGTAACAGCACCTCCCACGCGCTGCTGG  
TCCTGGTGCAGAAGCACATTAAAGCTGTCTTGAGTAACAAGCTGTGCCTGAGCATCTCCA  
ACCTGGTGCAGGGTGTCAATGTCCACCTGGGCACCTTAATTGGCCTCAACCCCGTGGGTG  
CTGAGTCCCAGATCCGCTATTCCATGGTCAGTGTGCCCACTGTCAACAGTGACTACATTT  
CCCTGGAAGTCAATGCTGTTCTCTTCCCTGCTGGGCAACCCCATCATCTGCCACGGATG  
CCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCTCCATGGCCACCGTGGGCC  
TCTCCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGGCCGGTGCCCTCAACC  
TGGACATCACAGGGCAGCTGAGGTCCGATGACAACCTGCTGAACACCTCTGCTCTGGGCC  
GGCTCATCCCGGAGGTGGCCCCGCCAGTTTCCCCGAGCCCATGCCTGTGGTGCTCAAGGTGC  
GGCTGGGTGCCACACCTGTGGCCATGCTCCACACAACAACGCCACCTGCGGCTGCAGC  
CCTTCGTGGAGGTCCTGGCCACAGCCTCCAACCTCGGCTTCCAGTCCCTCTTCTCCCTGG  
ATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA  
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATA  
CAGATCAGGTGCGCACACTGATGGGCACCGTTTTTTGAGAAGCCCCTGCTGGACCATCTCA  
ATGCTCTCTTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCC  
CTGAGATCTTTGTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCT  
GAGGCAAGACCACTGGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCA  
TTTCAAGCCACTGGGGAACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGAC  
TGCTTAGCTGGGCTGTTTTATCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCC  
CTTTCCCTTCCTCCTCCTCTTCTCCTCCCTCTTCCCTCATCTCCCCCTCCTTCCTCTGC  
CCCACCCAGGGGGAGCAGACTGCTCCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTA  
AACAACTTCTCTTGAGCTGC

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## FIGURE 322

MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFELDWS  
 GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPEPLELTLPVELLADT  
 RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIKAVLSNKLCLISISNL  
 VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSFYISLEVNAVLFLLGNPIILPTDAT  
 PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL  
 IPEVARQFPEPMPVVLKVRGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV  
 VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEKPLLDHLNA  
 LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS

### Important features of the protein:

#### Signal peptide:

Amino acids 1-20

#### Transmembrane domain:

Amino acids 217-236

#### N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

#### N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

#### LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

## FIGURE 323

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTTCTCAGGACCCTCGCCATGAA  
AGCCCTTATGCTGCTCACCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTG  
TCACTCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGA  
GCCAGGACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAA  
TCTGCGCTGTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAA  
GCTGGGTCTGACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACC  
CCGGCCCACTCCAGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTG  
GCTGCTGCACTGAGACTCATTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGC  
CTCTCTCCCTGTGTCTCTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCAT  
TTCTTTAATTAAACACTGTTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCT  
TCACTCTCCTTTTTCTGGGTCCCTTCCCACCTTCCCTTCCAGGACCTCCATTGGCTCCTAGA  
AGGGCTCCCCACTTTGCTTCCTATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATC  
TGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTGAAGGCTCCACAAGGACCTGATGA  
CCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCCATATGTACCCCATCCCCCATA  
CTCACCTCTTTCCATTTTGAGTAATAAATGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA



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## FIGURE 325

ACGGGCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTG  
CAGTCGGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCG  
CGCTACCGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAG  
CGCCATGGCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCA  
TTTGTTTCTGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCT  
GCGGGATGTAAAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGA  
TCCCATCCCACAGTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAA  
AGTCATACAGTGTGAGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGAC  
GGACTTAGATATTGCATACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTC  
CTCTGAAGACCAGTATGTACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATAC  
AGAACTTGGCCTGCAGAACTGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTCTC  
TGATTATTATTATAAGTGGTCCTCGGCGGATTCCTGTAAACATGAGTGGATTGATTACCAT  
CGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAAGCTGTTCTTGAGTGACGGGCAGTA  
TTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCACCGTTACCAGAGATTCACCAA  
CTCAGCAGGACCTCCTCCCCCAGGCTTTAAGTCTGAGTTCACAGGACCACAGAATACTGG  
CCATGGTGCAACTTCTGGTTTTTGGCAGTGCTTTTACAGGACAACAAGGATATGAAAATTC  
AGGACCAGGGTTCTGGACAGGCTTGGGAACTGGTGGAATACTAGGATATTTGTTTGGCAG  
CAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCTATCCTCCCTCCTA  
CCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTATTCCGGT  
ATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAGACG  
ATAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT  
CTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAGTTCT  
GTGGTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTG  
TGACAAAATACTTATGTGTTGTATGTGAGTGAACATGCAGATGTATATTGCAGTTTTTG  
AAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCT  
AAGAAGCATTAAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTTCAGTT  
TTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTAT  
TATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGC  
TAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTGAGTGGTGGAGA  
TGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGA  
AGGTTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTCGT  
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGT  
TCTCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

## FIGURE 326

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDP  
 IPQLKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCGYESS  
 EDQYVLRGSCGLEYNLDYTELGGLQKLKESGKQHGFAFSDYYYKWSSADSCNMSGLITIV  
 VLLGIAFVVYKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGQPQNTGH  
 GATSGFGSAFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSY  
 GTWNRAYSPLHGGSGSYSVCSNSDTKTRTASGYGGTRRR

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 171-190

**N-glycosylation site:**

amino acids 172-176

**Glycosaminoglycan attachment sites:**

amino acids 244-248, 259-263, 331-335

**Tyrosine kinase phosphorylation site:**

amino acids 98-106

**N-myristoylation sites:**

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
 270-276, 278-284, 312-318

## FIGURE 327

GGCACGAGGTGGAAGGGCTTTTACAAACAGATTGCTGGCCCCACCCCCAGAATTTCTCA  
 TCAGGAGTGGGCAAGACCAATCATTTGCATTTCTGACAAGTTCCCAGGAGCTGCAGCTGC  
 TGGCCCTGGAACCACACTTTGAGAACCACTGCTTTAGACCAAACACCAAAGGAAGATGCA  
 GCCACCCTCCTTTACATGTCACAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCT  
 GAGCTCCACCTGCAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGGCTAGGAGTGA  
 AGCGTGTCAACCATGGTCAGCTCATGGCCAGCCAGGAAAGCCTCTCTGCTGTGCGTCTGTG  
 CAGTTCTTGTTCTTCCCTGGAGGACTCTTGGATCGCCTGTGATCTTGGCCAGGAGACCAG  
 GTGCCTGGGTCCCTTCCTGGAAGGGGACAAGTTACACACCCCAGCCCCATTTTCCACCA  
 ACTTCTACATGCCTTGGGAGAACCTTCTACATGTTGGCTGCCCCCTTCCCCTATTTTACAGC  
 AGTGCCCAGTCCTGCTTATAAACCTGAGGCCTGCTCCCCATACCTTCCCTGTGCAAGTGC  
 CAGCCGTTATTCCAGGCAGCCCAATGTTGTTGAGGCCAGATGGATTCTTGAAGCAGCTG  
 GCCCATGGATGTGAGTCATCACAGTATTCTAGAAACAGAGAAGAGGTCTTAACCTAATGC  
 GCATAGAGAAATTGTTCTCATTGTAAACATACCCCTGTCCTTAGCTGATCTAGGTGGAAG  
 CCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAAAGGAATTGTATCTAGGACTAA

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## FIGURE 328

MVSSWPARKASLLCVCAVLVLPWRTLGSPPVILARRPGAWVPSWKGTSYTPQPHFPTNFYM  
PWENLLHVGCPPLPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLEAAGPWM

**Signal peptide:**  
amino acids 1-27

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**  
amino acids 8-12



# FIGURE 329

CAAAGAGTAGTCAGTCCCTTCTTGGCTCTGCTGACACTCGAGCCCACATTCCATCACCTG  
 CTCCCAATCATGCAGGTCTCCACTGCTGCCCTTGCCGTCCTCCTCTGCACCATGGCTCTC  
 TGCAACCAGGTCCTCTCTGCACCACTTGCTGCTGACACGCCGACCGCCTGCTGCTTCAGC  
 TACACCTCCCGACAGATTCCACAGAATTTTCATAGCTGACTACTTTGAGACGAGCAGCCAG  
 TGCTCCAAGCCCAGTGTCATCTTCCTAACCAAGAGAGGCCGGCAGGTCTGTGCTGACCCC  
 AGTGAGGAGTGGGTCCAGAAATACGTCAGTGACCTGGAGCTGAGTGCCTTGAGGGGTCCAG  
 AAGCTTCGAGGCCCGACGACCTCAGTGGGCCCAGTGGGGAGGAGCAGGAGCCTGAGCCTT  
 GGGAACATGCGTGTGACCTCTACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGC  
 CACACTGTGGGACTCTTCTTAACTTAAATTTTAAATTTATTTATACTATTTAGTTTTTATA  
 ATTTATTTTTTGATTTTCACAGTGTGTTTGTGATTGTTTGCTCTGAGAGTTCCCCCTGTCCC  
 CTCCCCCTTCCCTCACAGTGTGTCTGGTGACAACCGAGTGGCTGTCATCGGCCTGTGTAG  
 GCAGTCATGGCACCAAAGCCACCAGACTGACAAATGTGTATCAAATGCTTTTGTTCAGGG  
 CTGTGATCGGCCTGGGGAAATAATAAAGATGTTCTTTTAAACGGTAAAAAA

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## FIGURE 330

MQVSTAALAVLLCTMALCNQVLSAPLAADTPTACCFSYTSRQIPQNFIADYFETSSQCSK  
PSVIFLTRGRQVCADPSEEWVQKYVSDLELSA

Signal sequence:

1-23

Small cytokines (intercrine/chemokine) C-C subfamily

signature:

1-35, 2-36, 10-44, 34-74, 50-90

Small cytokines (intecrine/chemokine):

24-89

## FIGURE 331

GGCACGAGGTGAGACTTTAAATGAAATGTCTCACAGCTAGGTGATCCAGGTTTTGTGGT  
 CTTTGCAACCCTTGTGGTCATTGTGGCCTTGATATTAATCTTCGTGGTGGGTCCTCGCCA  
 TGGACAGACAAACATTCTTGTGTACATAACAATCTGCTCTGTAATCGGCGCGTTTTTCAGT  
 CTCCTGTGTGAAGGGCCTGGGCATTGCTATCAAGGAGCTGTTTGCAGGGAAGCCTGTGCT  
 GCGGCATCCCCTGGCTTGGATTCTGCTGCTGAGCCTCATCGTCTGTGTGAGCACACAGAT  
 TAATTACCTAAATAGGGCCCTGGATATATTCAACACTTCCATTGTGACTCCAATATATTA  
 TGTATTCTTTACAACATCAGTTTTAACTTGTTCAGCTATTCTTTTTAAGGAGTGGCAAGA  
 TATGCCTGTTGACGATGTCATTGGTACTTTGAGTGGCTTCTTTACAATCATTGTGGGGAT  
 ATTCTTGTGTGCATGCCTTTAAAGACGTCAGCTTTAGTCTAGCAAGTCTGCCTGTGTCTTT  
 TCGAAAAGACGAGAAAAGCAATGAATGGCAATCTCTCTAATATGTATGAAGTCTTAATAA  
 TAATGAAGAAAGCTTAACCTGTGGAATCGAACAACACACTGGTGAAAATGTCTCCCGAAG  
 AAATGGAAATCTGACAGCTTTTTTAAGAAAGGTGTAATTAAAGGTAAATCTGTGATTGTTA  
 TGAAGTGAATTTGAATATCATCAGAATGTGTCTGAAAAACATTGTCTCAAATAATGTT  
 CTTTAAAGGCAATCTTTTTAAAGATTTCACTAATTTGGACCAAGAAATTACTTTTCTTGT  
 ATTTAAACAAACAATGGTAGCTCACTAAAATGACCTCAGCACATGACGATTTCTATTAAC  
 ATTTTATTGTTGTAGAAGTATTTTACATTTTCATCCCTTCTCCAAAAGCCGAATGCACTA  
 ATGACAGTTTTAAGTCTATGAAAATGCTTTATTTTTTTCATTGGTGATGAAAGTCTGAAAT  
 GTGCATTTGTCATCCCCACTCCATCAATCCCTGACCATGTAAGGCTTTTTTATTTTAAAA  
 AAACAGAGTTATCCCAATACATTATCCTGTGATTTACCTTACCTACAAAAGTGGCTCCTG  
 TTTGTTTGATGATGATTGGTTTTATTTTTGAAATATTTATTAAGGGAAAACCTAAGTTACT  
 GAATGAAGGAACCTCTTCTTACAAAACAAAAAAGGGCAGAAATCACCCCAAGGAACG  
 ATTTCTCAGGTTGAGATGATCACCGTGAATCCGGCTTCCTCTGAGCATTCGATGGCCTTA  
 GCACCTCATCAAGCCAGCACATCCTGCCTGCTGTTGCAGCCTGGCTGGGTTTATTCTTCA  
 GTTACCCTAATCCCATGATGCCTGGAACCTTGATTACCGTTTTTACATCAGCTCTTGTACT  
 TTTCAGTATATTTTTCATAATGAGTTATATTGTCATTTAGACTTTGAACAGCTCTGGGAAA  
 TAGAAGACTAGGGTTGTTTCTTAAATTTAGCTCATGTTATAATAAAAAGTTGAAATG

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## FIGURE 332

MSHKLGDPGFVVFATLVVIVALILIFVVGPRHGQTNILVYITICSVIGAFSVSCVKGLGI  
AIKELFAGKPVLRHPLAWILLLSLIVCVSTQINYLNRLDIFNTSIVTPIYYVFFTTSVL  
TCSAILFKEWQDMPVDDVIGTSLSGFFTIIIVGIFLLHAFKDVSFSLASLPVSFRKDEKAMN  
GNLSNMYEVLNNNEESLTCGIEQHTGENVSRRNGNLTA

**Signal sequence:**

1-33

**Transmembrane domain:**

40-60, 70-90, 103-123, 139-159

**N-glycosylation site:**

103-106, 182-185, 208-211, 215-218

**N-myristoylation site:**

57-62, 140-145, 181-186, 214-219



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## FIGURE 334

MAAGDGDVKLGTTLGSGSESSNDGGSESPGDAGAAAEGGGWAAAALALLTGGGEMLLNVAL  
VALVLLGAYRLWVRWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNPRIL  
LAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLDKDALRDEYDDLSDLNAVQM  
ESVREWEMQFKEYDYVGRLLKPGEEPSEYTDEEDTKDHNKQD

**Signal sequence:**

None

**Transmembrane domain:**

45-65

**Tyrosine kinase phosphorylation site:**

202-210

**N-myristoylation site:**

11-16, 16-21, 37-42, 38-43, 79-84, 81-86, 83-88, 144-149

**Amidation site:**

75-78

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## FIGURE 336

TGRGYCGDHESSFGAMEEPGATPQPYLGLLLEELRRVVAALPEGMRPDSNLYGFPWELVI  
 CAAVVGFFAVLFFLWRSFRSVRSRLYVGREKKLALMLSGLIEEKSLLLEKFSLVQKEYEG  
 YEVESSLKDASFEKEATEAQSLEATCEKLNRSNSELEDEILCLEKELKEEKSXHSEQDEL  
 MADISKRIQSLEDESKSLKSQVAEAKMTFQIFQMNEERLKIAIKDALNENSQLOESQKQL  
 LQEAENVWKEQVSELNKKVTFEDSKVHAEQVLNDKESHIKTLTERLLKMKDWAAMLGEDI  
 TDDDNLELEMNSESENGAYLDNPPKGALKKLIHAAKLNASLKTLEGERNQIYIQLSEVDK  
 TKEELTEHIKNLQTQQASLQSENTHFENENQKLQKLVMTELYQENEMKLHRKLTVEEN  
 YRLEKEEKLKSKVDEKISHATEELETYRKRAKDLEELERTIHSYQGQIISHEKKAHDNWL  
 AARNAERNLNDLRKENAHRQKLTETELKFELLEKDPYALDVPNTAFGRGSRGPGNPLDH  
 QITNERGESSCDRLTDPHRAPSDTGSLSPWDQDRMMFPPPGQSYPDALPPQRQDRFC  
 SNSGRLSGPAELRSFNMPSLDKMDGSMPSSEMRNDTKDDLGNLNVPDSSLPAENEATG  
 PGFVPPPLAPIRGPLFPVDARGPFLRRGPPFPPPPPGAMFGASRDYFPPRDFPGPPPAPF  
 AMRNVYPPRGFPFPPYLPFRPGFFPPPPHSEGRSEFPFSGLIPPSNEPATEHPEPQQET

**Signal sequence:**

None

**Transmembrane domain:**

54-74

**N-glycosylation site:**

150-153, 338-341, 636-639

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

413-416

**Tyrosine kinase phosphorylation site:**

414-421

**N-myristoylation site:**

466-417, 625-630, 697-702

**Leucine zipper pattern:**

142-163



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## FIGURE 337

GGACTGCGGTCTCGGGCAGCAATGGCCGAGAAGCGCGACACACGGGACTCCGAAGCCCAG  
CGGCTCCCCGACTCCTTCAAGGACAGCCCCAGTAAGGGCCTTGGACCTTGCGGATGGATT  
TTGGTGGCGTTCTCATTCTTATTACCGTTATAACTTTCCCAATCTCAATATGGATGTGC  
ATAAAGATTATAAAAGAGTATGAAAGAGCCATCATCTTTAGATTGGGTGCGATTTTACAA  
GGAGGAGCCAAAGGACCTGGTTTGTATTTTATTCTGCCATGCACTGACAGCTTCATCAAA  
GTGGACATGAGAACTATTTCAATTTGATATTCCTCCTCAGGAGATCCTGACAAAGGATTCA  
GTGACAATTAGCGTGGATGGTGTGGTCTATTACCGCGTTGAGAAATGCAACCCTGGCTGTG  
GCAAATATCACCAACGCTGACTCAGCAACCCGTCCTTTGGCACAACTACTCTGAGGAAT  
GTTCTGGGCACCAAGAATCTTTCTCAGATCCTCTCTGACAGAGAAGAAATGACACACAAC  
ATGCAGTCTACTCTGGATGATGCCACTGATGCCTGGGGAATAAAGGTGGAGCGTGTGGAA  
ATTAAGGATGTGAACTACCTGTGCAGCTCCAGAGAGCTATGGCTGCAGAAGCAGAAGCG  
TCCCGCGAGGCCCCGCGCCAAGGTATTGTCAGCCGAAGGAGAAATGAATGCATCCAGGGCT  
CTGAAAGAAGCCTCCATGGTCATCACTGAATCTCCTGCAGCCCTTCAGCTCCGATACCTG  
CAGACACTGACCACCATTGCTGCTGAGAAAACTCAACAATTGTCTTCCCTCTGCCCAT  
GATATGCTGCAAGGAATCATAGGGGCAAAACACAGCCATCTAGGCTAGTGTAGAGATGAG  
CGCTAGCCTTCCAAGCATGAAGTCGGGGACCAAAATTAGCCTTTAACTCATAAAGAGAGGG  
TAGGGCTTTTCTTTTCCATATGTCAATTGTGGTGTGCCAGAAATGTATAGCAGTTATAA  
AAATAGGTGAAAGAATTGTTAGCTTGTAATACTGAGAGATTGGTGATTATATATAAGGTA  
ATCTGTTAGTCTTAAATAGTTAAAGTTTGTATTTTAGATTATTATGTAGTAGGTTAG  
ATCCCTCTTGTTTGGACTTCCACTGACTCATTCTGAACCCCTAAGCACCCAGGCCACAG  
GCAAGAACCTGGGCTGTAAGTCCACCTGACACCGCTGACTGGCTAAATGCTTTGCAGAA  
AGTGATGACCTTACACCACAACCAGCTTCTCCAGGTCATATGTGCCTTACCTCCAGAAGT  
CTTTTTTTTTTTTTTTTTTCTGAGATGGAGTTTCACTCTTGTTGCCAGGCTGGAGTGCAA  
TAGCATGATCTCGGCTCACTGCAACCTCCGCTCCTGGGTTCAAGAGATTCTCCTGCCTC  
AGCCTCCCCAGTAGCTGGGATTACAGGCTCATGCCACCATGCCAGCTAATTTTTGTATT  
ATTATTATTGTTTTTTAGTAGAGACGGGGTTTACCATTGTTGGCCAGGCTAGTCACGAAC  
TCCTAACCTCAGGTGATCCACCCACCTCTGCCTCCAAAGTGCTGGATTACAGGCTGAGCT  
ACCACCCTGGTTTGGAGAGTCTTAATTAATTGAAATTTCCCTAATGTTTATTTTCT  
AAATCCAGCGTGTTTTCAGAATAATCCTTACTTGAGAGTAGCCATTTTCTTGTTGTTACTTG  
TCAGAACTAGAGGAAATAGCCAAGACTAATGAAAAACATTACTCTAACCTTAAAAGACT  
TTTAAATTCACTACTAGAGTGGTCATTTTAAAAATACATCCATGTTTAACTTATTTTGA  
GCCTTTCTTTTATGAGTAAATGATTCTCCTGTTCTGTCTTTCAAACCAGCTAAATATT  
TGTCACAAAAGTGACTTTTTTCTCACTGTTGCCTATTTTCATATATCAGGTTTTAAATAG  
TTTTAATTTTTTAATAAAATTTTTCTCTACGTTCTATATGCAATTGTTATATATCTATTT  
GAATAGCTGAAGGACTAAAATACTTTTTTAAGAGATAACTTCAGGAAACCATTATATTTT  
ACTATCTGCATGCTGTAACTGTGGTACACTGTGAAATATGTTGATTACAAACCCATTCA  
TTACATAGTATAAGGAATTCACAGTATATTGACTATATAGTGTCTAATGACTGGGCAGAT  
ACTGTCAACTTACAATATCTATATAGAGAGGCTTTAACTTACCTTACTCATTCTCTATG  
ATGTATGACTTGATGCTGAAAGAGGAAGCTGGTCAGCTCCTCATGGACAACAAATTCTTA  
GTCTATAATATTAGGAGACATCTCTAGTTTTGCAAATGTCTGTGAATCTGAGCAACCTGG  
ACTTCTGCTTACTGGCCAGAAAGCTGGCGGGTGACATTTGTAACATTTCTCTTTGAGAC  
TCTGAGTTCACCTAGAGAAGTCTAAGCATAACAGCTTTCTTTCCAGCACGAGCCTTTAT  
AGCTCTCTTTAGCTCAACCACTCTGTCCATCCAGCCAATGGATGTCCTTCCCTGTACCCA  
ATTCAAGCTTATTTTAGGGAAGCCTTGAAACTACCATGTATCTGGCTCTAGCTGAGTTAT  
TGAGGATTGAGCCAGTGCAACGTTAAACTCAGTGCACCTTACATTTGATTTAAATGATGGT  
TTTATCTGTTGTGTGAAGTGGTTTACCCTTGAGGACCAGGAGCCTCCATATCCTGACTGA  
AAACCTTTTCTGAGACTTAGAGTAACAGTACTTTTGGTTTCTTGAGTTCTCCTGTCTCCA  
GATACCTAAATGACCTTGACTTTTCTGCCTTGTGAATTCGTAGTCCAATCAGCTGAAATTT  
AAATCACTTGGGAGGGACGCATAGAAGGAGCTCTAGGAACACAGTGCCAGTGCCAGAGTT  
TCTCCAGGTGGCCTCCCTTTCCAACAATGTACATAATAAAGTGTATGCACTTTCACT

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## FIGURE 338

MAEKRDTRDSEAQRLPDSFKDSPSKGLGPCGWILVAFSFLFTVITFPISIWMCIKIKEY  
ERAIIFRLGRILQGGAKGPGLFFILPCTDSFIKVD MRTISFDIPPQEILTKDSVTISVDG  
VVYYRVQNATLAVANITNADSATRLLAQTTLRNVLGTKNLSQILSDREEIAHNMQSTLDD  
ATDAWGIKVERVEIKDVKLPVQLQRAMAAEAEASREARAKVIAAEGEMNASRALKEASMV  
ITESPAALQLRYLQTLTTIAAEKNSTIVFPLPIDMLQGIIGAKHSHLG

**Signal sequence:**

1-45

**Transmembrane domain:**

None

**N-glycosylation site:**

128-131, 135-138, 159-162, 229-232, 264-267

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

4-7

**N-myristoylation site:**

26-31, 278-283, 281-286

**SPFH domain/Band 7 family:**

39-230

# FIGURE 339

TCTAGAGCCCTCTCCCAACATGGCGGCCTCAGCAAAAAAGAAGAATAAGAAGGGGAAGAC  
TATCTCCCTAACAGACTTTCTGGCTGAGGATGGGGGTACTGGTGGAGGAAGCACCTATGT  
TTCCAAACCAGTCAGCTGGGCTGATGAAACGGATGACCTGGAAGGAGATGTTTCGACCAC  
TTGGCACAGTAACGATGACGATGTGTATAGGGCGCCTCCAATTGACCGTTCATCCTTCC  
CACTGCTCCACGGGCTGCTCGGGAACCCAATATCGACCGGAGCCGTCTTCCCAAATCGCC  
ACCCTACACTGCTTTTCTAGGAAACCTACCCTATGATGTTACAGAAGAGTCAATTAAGGA  
ATTCTTTTCGAGGATTAAATATCAGTGCAGTGCCTTTACCACGTGAACCCAGCAATCCAGA  
GAGGTGAAAGGTTTGGTTATGCTGAATTTGAGGACCTGGATTCCCTGCTCAGTGCCCT  
GAGTCTCAATGAAGAGTCTCTAGGTAACAGGAGAATTCGAGTGGACGTTGCTGATCAAGC  
ACAGGATAAAGACAGGGATGATCGTTCTTTTGGCCGTGATAGAAATCGGGATTCTGACAA  
AACAGATACAGACTGGAGGGCTCGTCTGCTACAGACAGCTTTTGATGACTACCCACCTAG  
AAGAGGTGATGATAGCTTTGGAGACAAGTATCGAGATCGTTATGATTTCAGACCGGTATCG  
GGATGGGTATCGGGATGGGTATCGGGATGGCCACGCCGGGATATGGATCGATATGGTGG  
CCGGGATCGCTATGATGACCGAGGCAGCAGAGACTATGATAGAGGCTATGATTCCCGGAT  
AGGCAGTGGCAGAAGAGCATTGCGCAGTGGGTATCGCAGGGATGATGACTACAGAGGAGG  
CGGGGACCGCTATGAAGACCGATATGACAGACGGGATGATCGGTCTGAGCTCCAGAGA  
TGATTACTCTCGGGATGATTATAGGCGTGATGATAGAGGTCCCCCCCCAAGACCCAACT  
GAATCTAAAGCCTCGGAGTACTCCTGAAGAAGATGATTCTCTGCTAGTACCTCCCAGTC  
CACTCGAGCTGCTTCTATCTTTGGAGGGGGCAAAGCCTGTTGACACAGCTGCTAGAGAAAG  
AGAAGTAGAAGAACGGCTACAGAAGGAACAAGAGAAGTTGCAGCGTCAGTGGAAATGAGCC  
AAACTAGAACGACGGCCTCGGGAGAGACACCCAAGCTGGCGAAGTGAAGAACTCAGGA  
ACGGGAACGGTCGAGGACAGGAAGTGAGTCATCACAACTGGGACCTCCACCACATCTAG  
CAGAAATGCACGAAGGAGAGAGAGTGAAGAAGTCTCTAGAAAATGAAACACTCAATAAGGA  
GGAAGATTGCCACTCTCCAACCTCTAAACCTCCCCAACCTGATCAGCCCCCTAAAGGTAAT  
GCCAGCCCCCTCCACCAAAGGAGAATGCTTGGGTGAAGCGAAGTTCTAACCCCTCTGCTCG  
ATCTCAGAGCTCAGACACAGAGCAGCAGTCCCCTACAAGTGGTGGGGGAAAAGTAGCTCC  
AGCTCAACCATCTGAGGAAGGACCAGGAAGGAAAGATGAAAATAAAGTAGATGGGATGAA  
TGCCCCAAAAGGCCAAACTGGGAACCTTAGCCGTGGTCCAGGAGACGGAGGGAAACAGAGA  
CCACTGGAAGGAGTCAGATAGGAAAGATGGCAAAAAGGATCAAGACTCCAGATCTGCACC  
TGAGCCAAAGAAACCTGAGGAAAATCCAGCTTCTAAGTTCAGTTCTGCAAGCAAGTATGC  
TGCTCTCTCTGTTGATGGTGAAGATGAAAATGAGGGAGAAGATTATGCCGAAATAGACCTC  
TACATCCTGTGCTTTTCTCCTAGTTTCTCTCCACCCTGGAACATTCGAGAGCAAATCAAA  
ACCTCTATCCAGACAAGACAAAATAAACTCAACATCTCCTGAAGACCTTTCTTACCTTT  
TTTTAAAAACAAAAAXTGAAATTATTTTGCATGCTGCTGCAGCCTTTAAAGTATTGAAGT  
AACTGGAGAATTGCCAATACAGCCAGAGAGAAAGGGACTACAGCTTTTTTAGAGGAAAAGT  
TGTGGTGCCTTATGTCACCATGCAGTTGCCAGTGTGATTAGTGCCTAGGGGTCTCATTTA  
GCAGAAATGGTAATGACAGTGATATAATGCCTGGAACCTGGTTGGGCAGTAGGGGAGGGA  
GGTAGAAGGAAAAGTGTGAGATTTCTACCTTTTAGTTTTTCATCCTATTGTGGCATATATG  
AATTCTCAAACATTATCTGAATAAATTTTCCACTCTTGGAAGGTAGATTTAGCCTCAAG  
TTGTTCTAGTCTCCAGGAGGCTGCCAGCCCCCTCCTCTTATTTAATTCTGAGTTTTGGGGG  
CCAGCCTAGAGGGAATTCCTTTTTTTTTTTTTTTTAAACCCCCAGGGGGTAGTTGGGAGT  
GAGACTATAGGCCATAAAGAATGGGACTGCATTGGACCAAATAAATGGGAAAATCGTGG  
TTTGAAAAGAAGCTTTTGGGAAGTGATGAGTCATTTTGCACCAGGTAATAGGGGAAAATT  
GTGTGACCTCCAGCAAACACATGAATGGTTATTTCTGAGCCGGAAGCACTTGGGGGTC  
GTGGTAATTCCCAGTGTTTTCTGTGTCCTAGTTTTACCCTTTCTAAACACTGTCTTTTTT  
GAAAGTTTTGAATATATCCACATTCTATTGAAACCTTGAACTAAAAATTTAGACTCTTA  
TCGTCATCTTAAGTTCTTCATGCTACTCTTAACCTCCCCAAAAGCAGTATCTAAGTCACA  
TACATGATGTCTTGGGCATTTTCTGAGCCATGGAGAACTCTGAAAGGAAGAATCGCTGCT  
TTTCTCAAGCAAATCGGTTTCTTGATGTCTTTTGGTTCTCCTTGCTCCTGATGCTT

GGACCCCTTTTATTGATCAGAGTGCTCTAGAATAATGGATGGTCTTGGATGATGGATAAA  
TAGGGACAGGGACAGTTAAATTGGGAGCCTTTCTTACAACCTTGATGGGATTTTTCCCCC  
CAAGTTTCCTTCTCCACTGAAATGCCACACTAATGCTTGTTGGATTTCATGAGGTGGCCAG  
ACCAATGTGTTGTTTTGTTGTTGTTTTTTTTTTTAAAGCTTCCCTTGAGAGAATAAATGGTA  
ATGGAGAGAATCATTTAACAAGGTCCTGGTTTCTCTTGCAACACAGTAGCTAAACTTGCC  
TGCTTTTATATGCATTTTTGTAGGGATCAGCTTGGTAGACAGTATTAGCGGAGAAACACC  
TTGATCTTGGTTTGCAAGCCCTTCTCCCATCAGTCCTAGATTAGGCCCTGTTTCAGCCATG  
CAGGGGTGTTGGTTTATGCGTGCTGCAGCAGTGGGCATAATGAATATAATTTACCCAGTG  
GACAAAGGTGTGTACCAAGTGAATTTAAATAATTGGTGTGGATTGGCCAGTAGCTAAGAA  
GTGGGCTTTTAAAGAGTATTGAAGATTGAAAGGGTTTTTCTTTCTTTTTTAAAAAAGAAA  
AACAAACTATTGATTGTAGATAATGAAAAGCTAGGGTTTTGCCCTCTTCATGTCTACTCTC  
CTTCCAAATAGTTATATCCAAAACGTTTTTTCCCTCTCCCCTACCTTGTCCCCCCTATTA  
AAATAGAAACAGGGATTGATTAATGTCCCGCTCCTGAATACATGTAAAATTTGTACAAAA  
ATATCTTCTATGAAAATGATTTGTAATCTGTAGACTTATTACCTGGGAGATGTCTTGATG  
TAAAATCCCATCCTTTGGGTTGTGGGTTTTTTGTTTTCTCCAAATAAATCTGATCTTTAA  
AGTTAAAAAAAAAAAAAAAAACTCTAGAGTCGAGGAATTC

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## FIGURE 340

MAASAKKKKNGKGTISLTDFLAEDGGTGGGSTYVSKPVSWA  
 DETDDLEGDVSTTWHSNDD  
 DVYRAPPIDRSILPTAPRAAREPNIDRSRLPKSPPYTAFLGNLPYDVTEESIKEFFRGLN  
 ISAVRLPREPSNPERLKGFYAEFEDLDSLLSALSLSNEESLGNRRIRVDVADQAQDKDRD  
 DRSFGRDRNRDSDKTDTDWRARPATDSFDDYPPIRGDDSFQDKYRDRYDSDRYRDGYRDG  
 YRDGPRRDMDRYGGGRDRYDDRGSRDYDRGYDSRIGSGRRAFGSGYRRDDDYRGGGDRYED  
 RYDRRDRSWSSRDDYSRDDYRRDDRGPQRPKLNLKPRSTPEEDDSSASTSQSTRAASI  
 FGGAKPVDTAAREREVEERLQKEQEKLRQWNEPKLERPRERHPSWRSEETQERERSRT  
 GSESSQTGTSTTSSRNARRRESEKSLNETLNKEEDCHSPTSKPPKPDQPLKVMPAPPPK  
 ENAWVKRSSNPPARSQSSDTEQQSPTSGGGKVAPAPQSEEGPGRKDENVKVDGMNAPKGQT  
 GNSSRGPBGDGNRDHWKESDRKDGKKDQDSRSAPEPKPEENPASKFSSASKYAALSVDG  
 EDENEDEDYAE

### Signal Sequence:

None

### Transmembrane domain:

None

### N-glycosylation site:

120-123, 448-451, 542-545

### Glycosaminoglycan attachment site:

507-510

### cAMP- and cGMP-dependent protein kinase phosphorylation site:

439-442, 486-489

### Tyrosine kinase phosphorylation site:

225-233, 264-270

### N-myristoylation site:

25-30, 26-31, 28-33, 118-123, 421-426, 428-433, 538-543

### Amidation site:

276-279, 522-525, 563-566

### Cell attachment sequence:

215-217

### Eukaryotic putative RNA-binding region RNP-1 signature:

137-144

### RNA recognition motif:

98-168

## FIGURE 341

GCGTGGACACCACCTCAGCCCACTGAGCAGGAGTCACAGCACGAAGACCAAGCGCAAAGC  
GACCCCTGCCCTCCATCCTGACTGCTCCTCCTAAGAGAGATGCGCACCCGGCCAGAGCAGGA  
TTCTGCCCCCTTCTGCTGCTTCTGCTGCTGGGGCTGTGGGTGGCAGAGATCCCAGTCAGT  
GCCAAGCCCAAGGGCATGACCTCATCACAGTGGTTTTAAAATTTCAGCACATGCAGCCCAGC  
CCTCAAGCATGCAACTCAGCCATGAAAAACATTAACAAGCACACAAAACGGTGC AAAGAC  
CTCAACACCTTCCTGCACGAGCCTTTCTCCAGTGTGGCCGCCACCTGCCAGACCCCCAAA  
ATAGCCTGCAAGAATGGCGATAAAAACTGCCACCAGAGCCACGGGCCCCGTGTCCCTGACC  
ATGTGTAAGCTCACCTCAGGGAAGTATCCGAACTGCAGGTACAAAGAGAAGCGACAGAAC  
AAGTCTTACGTAGTGGCCTGTAAGCCTCCCCAGAAAAAGGACTCTCAGCAATTCCACCTG  
GTTCCCTGTACACTTGACAGAGTCCTTTAGGTTTCCAGACTGGCTTGCTCTTTGGCTGAC  
CTTCAATTCCCTCTCCAGGACTCCGCACCACTCCCCTACACCCAGAGCATTCTCTTCCCC  
TCATCTCTTGGGGCTGTTCCCTGGTTCAGCCTCTGCTGGGAGGCTGAAGCTGACACTCTGG  
TGAGCTGAGCTCTAGAGGGATGGCTTTTTCATCTTTTTTGTGCTGTTTTCCCAGATGCTTA  
TCCCCAAGAAACAGCAAGCTCAGGTCTGTGGGTTCCTGGTCTATGCCATTGCACATGTC  
TCCCCTGCCCCCTGGCATTAGGGCAGCATGACAAGGAGAGGAAATAAATGGAAAGGGGGC  
AA  
AAA

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## FIGURE 342

MAPARAGFCPLLLLLLLLGLWVAEIPVSAKPKGMTSSQWFKIQHMQPSPQACNSAMKNINK  
HTKRCKDLNNTFLHEPFSSVAATCQTPKIACKNGDKNCHQSHGPVSLTMCKLTSGKYPCNR  
YKEKRQNKSYVVACKPPQKKDSQQFHLVPVHLDRV

### Important features of the protein

**Signal peptide:**

1-22

**Transmembrane domain:**

none

**N-glycosylation site:**

127-131

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

139-143

**N-myristoylation site:**

18-24, 32-38

**Pancreatic ribonuclease family signature:**

65-72

**Pancreatic ribonuclease family proteins:**

49-93

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## FIGURE 343

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCCATGTGGC  
TGCCCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGT  
CTGTGAGAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGG  
AGACCTACATTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTG  
AAACCAGAGGGTCGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGA  
AAGACCGCACGTTCACTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACT  
GGTGTGGGATTGAAAGAAGAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACC  
CAGAGGGAGCGGCTTCCACAACAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTCA  
TCGGCTCCCAACAAGAGGAACCACTACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGC  
TCATCTTGGTCACTGCCATCCTCTGGTTGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAG  
GGGAACAGCCTATCTACATGAACTTCTCCGAACCTCTGACTAAAGACATGGCCACTTAGA  
GAGATGGATCTGCAGAGCCTTCCCTGCCCTGGCCACGTTTCCAGAAGAGACTCGGGCTGTG  
GAAGGAACATCTACGAGTCCTCGGGATGCAGTGACTGAGATAGGGGCCCTGGGCCTCCGC  
CCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCACAGCTCAGGGACTTAGCCAGGT  
CCTCTCCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTGTTCTCTTGGTCAGGAGCT  
GTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTGGAATAACTCGGGCAC  
AGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAGCCCTAGACTTCC  
ATCATTTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCCGTGTTTT  
TAAATTTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTCTAGGAAACCTCT  
CTGATCCCAACACAAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTATAGGCATGAGGG  
GCTGGATGGACCCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCA  
ATGGGAACCTCCCTGGCCCCGGCCGGTGTCTGTCTCCCCCTCCACCTCTTCTCCTCC  
TAGCTCCCCAAGCTCCCTGCCTATTCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTC  
CTCAGCATGACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTCAGGCCTCAAGAACCACCT  
CCAGGTGGGGAGGGCAGTAACGAAAACCATCGCAGGAAATGGCACCCCTCCCTTTTCGGTG  
ATGTTGAAATCATGTTACTAATGAAAACCTGTCTAGGGAAGTGGTTCTGTCTCCTCACAG  
GCTTCACCCACGGCGATGAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGA  
CCCTCACACCAAAGGGACCTTCCCATGTGAGATGTGCTCCCGCCCCACCTGCCACAAAG  
CAAACACACCACACATGTTTCGGCATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAAC  
CTGCTCTTGGTTCTAATAGGGAGTACTGACTGTGAGCAGTGGATAAAGGAGAGGGGACCC  
TCTGGTCCCTAGCATGGCACCCAGAGCCTCCCCCTCTTCTTGTCTTCAGCCAAAGAGAAA  
CTTTCTCTGACTTTGAACTGAATTTAGGTCTCTGGCCAATGATGGGCCTGAAAATTCCAT  
AATGGCCAGAGAGGAGAGTTCGAGCCCGGCTAAGATCCCCTGAGTCATTCTGTGAGGGAC  
CAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCCTGGAATGCTTTCCTGGATCCAG  
CTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGCTCCGCGGGAGGGAAAGCCA  
AAGCATGGTGCTTCACCAGCTGGACTCAGGGGCGAGGGGACATGGGCGCTTGTCAACGTG  
ATGTCATTCTTTTCCACCGTTTCTTCTGTTGATATTCAATGAATCCGTCAATCTCTCT  
GGGAAA



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## FIGURE 344

MWLPPALLLLSLSGCFHSIQGPESVRAPEQGSITVQCHYKQGWETIYIKWWCRGVRWDTCKI  
LIETRGSEQGEKSDRVSIKDNQKDRTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI  
VDPEGAASTTASSPTNSNMAVFIGSHKRNYMLLVFVKVPILLILVTAILWLKGSQRVPE  
EPGEQPIYMNFSPLTKDMAT

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-17

**Transmembrane domain:**

Amino acids 151-170

**N-glycosylation site:**

Amino acids 190-194

**Tyrosine kinase phosphorylation site:**

Amino acids 95-103

**N-myristoylation sites:**

Amino acids 66-72; 125-131

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 5-16

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## FIGURE 345

CTGAGCTCCCGGGCTCCGGCAGCGCGCTGGCGGGGCGCCGCATTGCACACTCTGGGGGCG  
CCGCAGTGTTTCGTGGGATGGGGCAGCGGGCTGCAGCTGGCGGGCCGGAATCCGCGCGCAGC  
CCGGGTGCAAGTTCTCTCCTGTTGCCCTGAGTGCCCACTCCCAGGCCCTCTGTATGAGTG  
ACACTTCAGTCTGCCATGGAACCTGGCCCTGCTCTGGCCTGGCTCCTGCTCCTGAGCCTG  
CTGGCGGATTGTCTGAAAGCTGCTCAGTCCCAGACTTCACAGTGAAAGACATTATCTAC  
CTCCATCCTTCAACCACACCATATCCTGGTGGATTTAAATGTTTCACCTGTGAAAAGGCA  
GCAGACAATTATGAGTGCAACCGATGGGCTCCAGACATCTACTGCCCTCGAGAGACCAGA  
TACTGCTACACTCAGCACACAATGGAAGTCACAGGAAACAGTATCTCAGTCACCAAACGC  
TGTGTCCCCTGGAAGAGTGCTTATCCACTGGCTGCAGAGACTCCGAGCATGAAGGCCAC  
AAGGTCTGCACTTCTTGTGTGAAGGAAATATCTGTAACCTTGCCACTGCCCCGAAATGAA  
ACTGATGCCACATTTGCCACGACGTCACCTATAAATCAGACAAATGGGCACCCACGCTGT  
ATGTCAGTGATAGTGCTTGTGGTTGTGGTTAGGGCTCATGTTATAGTGGCTCAGT  
GGCTCCATGTGTTAATAGCGATCCATGGGGATCTCGATGGTCCACAGACCTGCATGAGTC  
ATTGGCCTGACAGTAATTACACATGTGAGACACAACACTCTTGGAGGTCATCACAGCCAA  
GCATTGCCACTTACCATGAGGAATAAATGTTGCTTCATTGTAGCCATTTTGAGTCTAACC  
GAGACTCATCAAAGCCTTCTGTCAGTACAGCCCAAGTTCATACCATAAACGTTTGT  
CATTCCAAGAAGTAGTTCTGCATTTATCGAGATCTGGGGTCTTAATTTGGAAGAATACA  
TGCATGAGATGCAGTAGGTCCTGAGACTGTAAGATATTAGGAGTATGTTATAGGGGCATG  
TATAGATGTGGGCTTTTCAGGAGAAAAGTAACCATTGGTTTAAATATAATCATGAGTTCA  
TTTGTAGCTTTAGAATTTTAAACATTGACTCCAACTGAATGGACTATTTCTCTGGAAA  
TTCTGACTGAGTCCCTGGAAGAGTAGTAATTCCAACAATTCAGCCATTTGTTCAATTAA  
TTTTCCCAACATTCTTCTCCAGTGCTGGGAATCACATTTCTCTGTCTGTGCAGAAGA  
CAAAAAGGCAATCATAAAAGTTTGTATATTGTGGGGTGCCTGGAGGAGGATTTTCCT  
CAACTTAATGGAGCCACTGTCCATAAAGTGGCTGTTATCCCTTCATATAATTGGTGAGAT  
CAGCCTTCTCCTTGACTTGGCACCTAATTATGCTTCATGAGATCCTAGATTCCACCTGAG  
TCAATTGTGTCCAGAGCCCCAAACCAGGATGGAGTTGTTTTCCCCAGATATGGGGTTCTA  
TTCAGCCATAGATAATCTAGACAGAGGATTTCAGAATGAAAGGAAAAATGTGTGGAGATT  
AGTCCTAGTTCATTCTGAGGGCCGACTAAGTGGCTCAGCCAGCTTCTTACTCCATCTGCA  
GTTTCATACTGCCAAAGAGCTCCCACTTCCAAATCCCCAGTGACTTTTATGGAGAAGATTCT  
GCATTAAATTGTCTTTTGAATGATGGGGAAGCAAGGCATAATATGCGATGATGAGGAGAA  
AGTAGACCAGTGAGGTGATTGCAAGACTAACAAGGAGACTCAATGGGAAGTTTTTCTTTC  
TTTTAGATATTGCTTTTGAAGTAGATGGTAAATTTTTGTATCCTTCTTGTATTTTTTG  
TACCCCAAGTTACAATTTTTCTTCTTCTTGTAAATAATTTAAACAGTATTTATTTTTGT  
AAGGCATAACTAGAACTAAAATATATTCTAAAAAATTCATTATTCTGAACAAAGTGATC  
AAATTAGAATACATATTTTTCAACAGTGGTAGAGCTTTTAAATATATGTTTATTGAAAGTT  
ATCTATAATACTTGCACCAGTGTTGAAAAAAGTTAACATGTAGGCAAGAGCAATATGTTT  
GTCTCAAGGATTTTTCCATGGTTTTCTCAGTGATGGTGTCTGGAATTATTCAGGTGGTG  
ACCATCACTGGTCTAAGTTTGTGTGCAGGGTTTTTCAGACGTGTTTTTGTGAACTTGGTA  
GAACCATGGCTAATAAAGAGGACAGTGTTGTGAGGGTCCATCTGCCCTCCATAGAAAAAT  
GTCTCTGGCTCATAAAATGAGACTCCCTCAGGGACTAAATATGAACTGACAGCAGTAACCT  
CTGATACAGAATAATCTAAATTGCATCAAATGGCCTTAATTCAGAGTTTGTTAGGCTTAT  
CAGTATGTTGCTTTTAAATTGGGGTGGGAAAGTAGAGGGAGAGAAAGCAAGACATTTATTA  
AGCACCTCGTATGTGCCAGGCACTATGCTAAGCACTTTACATAAGTTAGGATTAATCCCT  
GCAAGAATCCTATAAAGAATGTTACTAGCATTTACACTTCCCAAATGAAGGTACCAAAGC  
TCAAACGCAATGTTGTGAAGCTGTTTCTTTCAGATTTAGGTTATGTGGGATGATGTGGGA  
TTGAAGAGGAAAGAAAGGTGGGATTATCCCCCTAGGAAGACTTTTCAGGCCTGACTTCATA  
GGAATTCATCCATCTTATCATGTGGAGTTTATCTCACCTGCTGTTGCAGGATGCTATTT  
GCATGTGTCCCAGGTGATGTTTTTCTTGGGGAGTAGGGGTTTGGCTTCCTCATTCAT

CCCTCTTGCTAAAAAGAGGAGATAGTTGATGTTGCATCTAAAGATGCTATAAGACAATGAAAGTTTGATGTTGTAC  
ATACCTACAAGTACCATTTTTTGTGCATGATTACACTCCACTGACATCTTCCAAGTACTAC  
ATGTGATTGAATAAGAAACAAGAAAGTGACCACACCAAAGCCTCCCTGGCTGGTGTACAG  
GGATCAGGTCCACAGTGGTGCAGATTCAACCACCACCCAGGGAGTGCTTGCAGACTCTGC  
ATAGATGTTGCTGCATGCGTCCCATGTGCCTGTCAGAATGGCAGTGTTTAATTCTCTTGA  
AAGAAAGTTATTTGCTCACTATCCCCAGCCTCAAGGAGCCAAGGAAGAGTCATTCACATG  
GAAGGTCCGGGACTGGTCAGCCACTCTGACTTTTCTACCACATTAAATTCTCCATTACAT  
CTCACTATTGGTAATGGCTTAAGTGTAAGAGCCATGATGTGTATATTAAGCTATGTGCC  
ACATATTTATTTTTAGACTCTCCACAGCATTTCATGTCAATATGGGATTAATGCCTAAACT  
TTGTAAATATTGTACAGTTTGTAATCAATGAATAAAGGTTTTGAGTGTAATAAAAAAAAAA  
AAAAAA

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## FIGURE 346

MEPGPALAWLLLLSLLADCLKAAQSRDFTVKDIIYLHPSTTPYPGGFKCFTCEKAADNYE  
CNRWAPDIYCPRETRYCYTQHTMEVTGNSISVTKRCVPLEECLSTGCRDSEHEGHKVCTS  
CCEGNICNLPLPRNETDATFATTSPINQTNHGPRCMSVIVSCLWLWLGLML

### Important features of the protein:

#### Signal peptide:

1-22

#### Transmembrane domain:

None

#### N-glycosylation site:

134-138, 147-151

#### N-myristoylation site:

45-51, 87-93, 106-112, 124-130

#### Ly-6 / u-PAR domain protein:

115-128

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## FIGURE 347

GATCAAGCGCCTTCCTTTCCCTTCCTCTCCCTACTTGGCCTTTGCCCTAAGCCAAGACCT  
GGCCATCAGCCTGGCTGCAGGGGCCTGCAGAGCCAGCTGCACTTTTTTCAGGTATGGGGGA  
GGGCCAGGCACCA**ATGA**AGCCAGTGTGGGTGCGCACCCCTTCTGTGGATGCTACTGCTGGTG  
CCCAGGCTGGGGGCCGCCCGGAAGGGGTCCCCAGAAGAGGCCTCCTTCTACTATGGAACC  
TTCCCTCTTGCTTCTCCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG  
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTCTTCACACACAGTGGGAAGGGGAAA  
GTGCTTGGAATGAGACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGAC  
ATCATTCTGCTGAGGGAACTGCACGTCAACCACTACCGATTCTCCCTGTCTTGCCCCGG  
CTCCTGCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGAATCGAATTCTACAGT  
GATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGCACCACTGG  
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAAC  
TACTTCAGAGACTACGCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGG  
ATCACGTTCAAGTATCCTCGGGCAATGGCAGAAAAAGGCTATGAGACGGGGCCACCATGCG  
CCGGGCCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACACCACATCATTAAGGCC  
CACGCCAAAACCTGGCATTCCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG  
GGAATTTCACTGAACTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTA  
GAGGCTGCCGAGAGATACCTACAGTTCTGTCTGGGCTGGTTTGCCAACCCCATTTATGCC  
GGTGACTACCCCAAGTCATGAAGGACTACATTGGAAGAAAGAGTGCAGAGCAAGGCCTG  
GAGATGTCGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTACATTAAAGGCACATCC  
GATTTCTTGCGATTAGGTCATTTTACTACTCGGTACATCACGGAAAGGAACCTACCCCTCC  
CGCCAGGGGGCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTTGACCCAAACTGG  
CCAGATCTGGGGTCTAAATGGCTATATTCTGTGCCATGGGGATTAGGAGGCTCCTTAAC  
TTTGCTCAGACTCAATACGGTGATCCTCCCATATATGTGATGGAAAATGGAGCATCTCAA  
AAATTCACCTGTACTCAATTATGTGATGAGTGGAGAATTCAATACCTTAAAGGATACATA  
AATGAAATGCTAAAAGCTATAAAAAGATGGTGCTAATATAAAGGGGTATACTTCCTGGTCT  
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTT  
GAATTTAACGACAGAAATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAG  
ATTATCATTGCCAATGGGTTTCCCAATCCAAGAGAGGTGGAAAGTTGGTACCTCAAAGCT  
TTGGAAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCTTTGCTAAGTCACATG  
CAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGTCCTCATCACTGCT  
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCT**GA**GACAGGATTATCAATTTTGAGCT  
TCATAAGAGAATCTTCAGGATCTTCCTCCCTTTTCTGCTTTGAGGGTTTCCATACATTGC  
TGTTTTCAGGTTCTACAATAATTACCTTTTTTTCTCTTTCTCTTTTGGCTTGTGCTGGG  
ATTTAAGAATTAGAAAATAAAAATAAGCAGAAATTA

## FIGURE 348

MKPVVWVATLLWMLLLVPRLGAARKGSPEEASFYYGTFPLGFSWGVGSSAYQTEGAWDQDG  
 KGPSIWDVFTSHSGKGKVLGNETADVACDGYKQVEDIILLRELHVNHYRFSLSWPRLLPT  
 GIRAEQVNKKGIEFYSDLIDALLSSNITPIVTLHHWDLPQLLQVKYGGWQNVSMANYFRD  
 YANLCFEAFGDRVKHWITFSDPRAMAEKGYETGHHAPGLKLRGTGLYKAAHHIIKAHAKT  
 WHSYNTTWRSKQQGLVGLSLNCDWGEPVDISNPKDLEAAERYLQFCLGWFFANPIYAGDYP  
 QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSIIKGTSDFLGLGHFTTRYITERNYPSRQGP  
 SYQNDRDLIELVDPNWPDLGSKWLYSVPWGFRRLLNFAQTQYGDPIIYVMENGASQKFHC  
 TQLCDEWRIQYLKGYINEMLKAIKDGANIKGYTSWSLLDKFEWEKGYSDRYGFYYVEFND  
 RNKPRYPKASVQYYKKIIANGFPNPREVESWYLKALETCSINNQMLAAEPLLSHMQMVT  
 EIVVPTVCSLCVLITAVLLMLLLRRQS

### Important features:

#### Signal peptide:

amino acids 1-21

#### Transmembrane domain:

amino acids 541-558

#### N-glycosylation sites:

amino acids 80-84,171-175,245-249

#### Glycosaminoglycan attachment site:

amino acids 72-76

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 23-27,564-568

#### Tyrosine kinase phosphorylation sites:

amino acids 203-211,347-355,460-468,507-514

#### N-myristoylation sites:

amino acids 44-50,79-85,167-173,225-231,257-263,315-321

#### Amidation site:

amino acids 307-311

#### Glycosyl hydrolases family 1 active site:

amino acids 407-416

#### Glycosyl hydrolases family 1 N-terminal signature:

amino acids 41-56

#### Motif name Glycosyl hydrolases family:

amino acids 37- 67

## FIGURE 349

CGCAAAGCCGCCCTCGGGGCGCTCATGGCGGGACGCCTCCTGGGAAAGGCTTTAGCCGCG  
 GTGTCTCTCTCTCTGGCCTTGGCCTCTGTGACTATCAGGTCTCGCGCTGCCGCGGCATC  
 CAGGCGTTCAGAACTCGTTTTTCATCTTCTTGGTTTTTCATCTTAATACCAACGTCATGTCT  
 GGTTCCTAATGGTTCCAAAGAAAATTCTCACAATAAGGCTCGGACGTCTCCTTACCCAGGT  
 TCAAAAGTTGAACGAAGCCAGGTTCTAATGAGAAAGTGGGCTGGCTTGTGAGTGGCAA  
 GACTATAAGCCTGTGGAATACACTGCAGTCTCTGTCTTGGCTGGACCCAGGTGGGCAGAT  
 CCTCAGATCAGTGAAAGTAATTTTTCTCCCAAGTTTAAACGAAAAGGATGGGCATGTTGAG  
 AGAAAGAGCAAGAATGGCCTGTATGAGATTGAAAATGGAAGACCGAGAAATCCTGCAGGA  
 CGGACTGGACTGGTGGGCCGGGGCTTTTGGGGCGATGGGGCCCAAATCACGCTGCAGAT  
 CCCATTATAACCAGATGGAAAAGGGATAGCAGTGGAAATAAAATCATGCATCCTGTTTTCT  
 GGAAGCATATCTTACAATTTGTTGCAATAAAAAGGAAAGACTGTGGAGAATGGGCAATC  
 CCAGGGGGGATGGTGGATCCAGGAGAGAAGATTAGTGCCACACTGAAAAGAGAATTTGGT  
 GAGGAAGCTCTCAACTCCTTACAGAAAACCAGTGCTGAGAAGAGAGAAATAGAGGAAAAG  
 TTGCACAAACTCTTCAGCCAAGACCACCTAGTGATATATAAGGGATATGTTGATGATCCT  
 CGAAACACTGATAATGCATGGATGGAGACAGAAGCTGTGAACTACCATGACGAAACAGGT  
 GAGATAATGGATAATCTTATGCTAGAAGCTGGAGATGATGCTGGAAAAGTGAAATGGGTG  
 GACATCAATGATAAACTGAAGCTTTATGCCAGTCACTCTCAATTCATCAAACCTTGTGGCT  
 GAGAAACGAGATGCACACTGGAGCGAGGACTCTGAAGCTGACTGCCATGCGTTGTAGCTG  
 ATGGTCTCCGTGTAAGCCAAAGGCCACAGAGGAGCATATACTGAAAAGAAGGCAGTATC  
 ACAGAAATTTATACTATAAAAAGGGCAGGGTAGGCCACTTGGCCTATTTACTTTCAAACA  
 ATTTGCATTTAGAGTGTTTCGCATCAGAATAACATGAGTAAGATGAACTGGAACACAAAA  
 TTTTCAGCTCTTTGGTCAAAAGGAATATAAGTAATCATATTTTGTATGTATTCGATTTAA  
 GCATGGCTTAAATTAAATTTAAACAATAATGCTCTTTGAAGAATCATAATCAGAATAAA  
 GATAAATTCTTGATCAGCTATA

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## FIGURE 350

MAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAFRNSFSSSWFHLNTNVMMSGSNGSKEN  
SHNKARTSPYPGSKVERSQVPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNF  
SPKFNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGPNAADPIITRWKR  
DSSGNKIMHPVSGKHILQFVAIKRKDCGEWAI PGGMVDPGEKISATLKREFGEEALNSLQ  
K TSAEKREIEEKLHKLF SQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLML  
EAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEK RDAH WSEDSEADCHAL

### Important features of the protein:

#### Signal peptide:

1-20

#### Transmembrane domain:

None

#### N-glycosylation site:

55-59

#### cAMP- and cGMP-dependent protein kinase phosphorylation site:

179-183

#### N-myristoylation site:

53-59, 56-62

#### mutT domain signature:

215-235



# FIGURE 351

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGG  
GCATGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTG  
AGCTGGCCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGT  
GGCCCCCTTGGCATTTCACACAAGACGCCAAGATGGAGATTCCCATGGGGACCCAGGGCTGC  
TTCTCAAAGAGCCTCCTGCTCTCAGCCTCAATCCTGGTCTCTGGATGCTCCAAGGCTCC  
CAGGCAGCTCTCTACATCCAGAAGATTCCAGAGCAGCCTCAAAGAACCAGGACCTTCTC  
CTGTCAGTCCAGGGTGTCCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAG  
ACGTACGGAGGCACGAGGCTATTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGAT  
GGCAGTGCCATGGGACAGCGAGACATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGC  
CGCGCCCAGCCTACAGACAGTGGCACCTACCAAGTAGCCATTACCATCAACTCTGAATGG  
ACTATGAAGGCCAAGACTGAGGTCCAGGTAGCTGAAAAGAATAAGGAGCTGCCCAGTACA  
CACCTGCCCACCAACGCTGGGATCCTGGCGGCCACCATCATTGGATCTCTTGCTGCCGGG  
GCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTGACAAGGAAGTGGAGGGGGCCAGAGC  
CACAGACTGCCTGCTCCGAGGGGCCAGGGATCTCTGTCCATCTTGTGCTCGGCTGTATCC  
CCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACAGAGAAGCCAGAATTGGGC  
CCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCCTCTCCAGTCTCTCTG  
GTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCCGCCCCCTGCCACACCCCCA  
CACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAACCCCGACCCT  
GCCCCCTACTGCCAGCTGGTGCCAACTTCCATGGGTCTCTGGGCCAGGCCAGCCAGGGA  
GAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAGGCC  
ATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA  
GGTGTCTTGGCAGGGGGACAGGAGACTGTAAACAGGCCCAGGTCCTTGTGCAGCCCCTGAA  
TGCACGCCCCGCTTCGGTCTGTTTCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAA  
AGGCAGGCTCTGGCCCCCTTCCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAA  
GATGGTGGCCTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCCTCA  
ATGCCCTACCCCAACTCCACTAGTGACCCTCAGAGTCTTCTCCCCTTAGGACAAGGCAGA  
CACCCACCATGCGGGCCTCAGGTGGCAGAGAGGCCAGCCTCACAGGCCTGTGGCCCCA  
CACACCAGTCCCAGCAAGGTGACCACGGCTGCTGGACCCCTTCCCTGTTTACGGCAGGCC  
AGCCCCCTCTCAGAACCTGCTGCCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGA  
GTCCCTCTGGGCAGCAGCTCCCTTCTCCACCCACCCAGCACCCGTCCCAAATGTGGCC  
TCAGCTTGCTCCTCCCCTTCCCCAACTATGCATTCATTACGCAATAAATGAGCCTTTGCT  
GCA

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## FIGURE 352

MEIPMGTQGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF  
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFNGSMLLRRAQPTDSGT  
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPTNAGILAATIIGSLAAGALLISCIAYL  
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGDAGDNNI  
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDPAPYCYLVPTS

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-32

**Transmembrane domain:**

Amino acids 159-178

**N-glycosylation site:**

Amino acids 104-108

**N-myristoylation sites:**

Amino acids 6-12; 29-35; 55-61; 91-97; 157-163; 165-171

# FIGURE 353

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATG  
GCCGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTC  
CTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGG  
CTTGACAAGTCCAACCTTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAG  
GAGGCTAGCTTGGCTGATAACAACACAGACGTTCTGTCTCATTGGGGAGAACTGTTCCAC  
GGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACCTTCACCCTTGAA  
GAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTC  
CTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATC  
CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATC  
AAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTGACCA  
GAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATG  
CCCCAAAGCGATTTTTTTTAAACCAAAGGAAGATGGGAAGCCAACTCCATCATGATGGG  
TGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAACTGG  
TGTTCTATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTTTCCATAAAAAAGAT  
TACTTTCCATTCCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTA  
CTTTATATTTATAAATGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTT  
ATTAATATGGATTTATTTATAGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAA  
TATTGATATTTATGACAATAATTATAGAGCTATAACATGTTTATTTGACCTCAATAAACA  
CTTGATATCCC

Prokaryotic membrane lipoprotein lipid attachment site:

# FIGURE 355

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAA  
**CAT**GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGT  
 CCCGGGCCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGA  
 CGAAGAGTGCAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGA  
 TTGTCGTTTTTGTGAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAAACTGGCAGG  
 GGGATCCCTTGAACTTTGGGCTGGAAGTGTGGAACACAGTTTTTGGATATTTTCCAAAAGA  
 TTTGATCAAGGTACTTCATAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGAC  
 AGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATTTTAAATAGTTATAATGTAGAAGAGCT  
 TTTAGGATCTTTGGAACCTGGAGGACTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGT  
 TTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGAACCTTGACCCTGTGCC  
 TGAGCCCGAGGCATTCAGAGCTGATTCAGAGGATGGAGAAGGTGCTTTCTCAGAGAGCAC  
 CGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGTCCTGC  
 GGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA  
 ATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCG  
 GGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACA  
 GTGCGTTATTATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGTTTTACAA  
 AGATTGTTTTT**TAG**TACTAAGCTGCCTTGGCAGTTTGCATTTTGGAGCCAAACAAAATAT  
 ATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 356

MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD  
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLH KYTEELHIPADET  
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSP EESRGRELD PVP  
EPEAFRADSEEDGEGAFSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDK  
LKVPGSESRTGNSSPASVEREKTDAYKVLKTEMSQ RSGSGQCVIHYSKGFRWHQNL SLFYK  
DCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site:**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 30-34

**Tyrosine kinase phosphorylation site:**

amino acids 67-76

**N-myristoylation sites:**

amino acids 205-211, 225-231, 277-283

**Amidation site:**

amino acids 28-32

[illegible]

N-myristoylation site:



# FIGURE 359

TTCCAGTCAGAGTTAAGTTAAAACAGAAAAAAGGAAGATGGCAAGAATATTGTTACTTTT  
 CCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGAATATTTATGGACCGTCTAGCTTC  
 CAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACTATTTCTCTGGCTAGTGCTCAAGA  
 AGATTATAATGCCCCGACTGTAGATTCATTAACGTTAAAAAAGGGCAGCAGATCTATGT  
 GACTCAAAGCTGGTAAAAGAAAATGGAGCTGGAGAATTTTGGGCTGGCAGTGTTTATGG  
 TGATGGCCAGGACGAGATGGGAGTCGTGGGTATTTCCCCAGGAAC TTGGTCAAGGAACA  
 GCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCACACGGATATTGACTTCTTCTGCGA  
GTAAATAATTAGTTAAAAC TGCAAATAGAAAGAAAACACCAAAAATAAAGAAAAGAGCAA  
 AAGTGGCCAAAAAATGCATGTCTGTAATTTTGGACTGACGT

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## FIGURE 360

MARILLLLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTISLASAQEDYNAPDCRFINV  
KKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVG YFPRNLVKEQRVYQEATKEVPT  
TDIDFFCE

Important features of the protein:

Signal peptide:

1-14

Transmembrane domain:

None

N-myristoylation site:

84-90

# FIGURE 361

GGCACGAGCCACCACTTACAACCACACAGCCTATCCAGAAACATGAAGATAAGAAATGCT  
TGTGCTGTCCTTATTGAAGTACTCCTGTTTATACTTGAAGGAGTTACAGGAGCTCGAAAA  
ATTTCAACTTTCTCAGGCCCTGGCTCATGGCCGTGCAATCCCAAGTGTGATGGCAGAACT  
TACAACCCCTCAGAGGAGTGTTGTGTTTCATGACACCATCCTGCCCTTTAAGCGGATTAAC  
CTCTGTGGCCCTAGCTGCACCTACAGGCCCTGCTTTGAGCTCTGCTGTCTGAGTCCTAT  
AGCCCCAAGAAGAAATTTATTGTCAAGCTTAAAGTTCATGGAGAGAGATCCCATTGCAGT  
TCATCCCCTATCTCCAGGAAGTGTAAAAGCAACAAGATTTTTTCATGGAGAAGATATTGAA  
GACAACCAACTTTCTCTTAGGAAAAAAAGTGGTGACCAGCCTTGAAGAGTCTGCTTTCTTC  
CTGCAAGCACCAGTTCCTGAATGTTCTTACTTGAAGAATGGATACCTGAAGCATTGGGGT  
GCAGTGATATATGTGTCTCATTACAATGCTCCTTTGGATATTGTTTTCTAAGCATGTGT  
TGGAATGTTCCCCCATAACTTTCTAAAATTATCCTATTTCAATGCAACTAAAGATAAATG  
TATTCCAGCCAGAGTCCACAGAGAAGGCAAGTTATGCAAGGCAGGCATGGGGCCCTCACA  
AAATTTCAAGCTGTGCGACTTATGTAGTAATTTTCTACAAACAATCCCTCCTGGATATCC  
AGGAGGCTCCAGACCTGAATAAAAACCATGTCTGTCTAGAAAAAGGGAATGAATCAAG  
ATCCACAGGACCTTTTCAAGATTTTGAAGCAGCAAACTATGGCTGAGAGAAAAGACTCT  
CTGACCAGGCAAATTGTTCTGCAGTATTCTCCGGGCGTGTAGCTCCCCTGAGTAGTCGCC  
AGGCTGGTCTTGGCTTTGTAATAATACAGCTGCCTTTGAGTCCTCCCTACCCTGTTAGTA  
ACCCCTTGCCTGCACTGTTGTCCTTACAACCGAAATAAACTGATTAGTTG

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## FIGURE 362

MKIRNACAVLIEVLLFILEGVTGARKISTFSGPGSWPCNPKCDGRTYNPSEECCVHDTIL  
PFKRINLCGPSCTYRPCFELCCPESYSPKKKFIVKLKVHGERSHCSSSPISRNCKSNKIF  
HGEDIEDNQLSLRKKSGDQP

Important features of the protein:

Signal peptide:

1-23

Transmembrane domain:

None

Glycosaminoglycan attachment site:

31-35

N-myristoylation site:

20-26, 34-40

# FIGURE 363

A C A C T G G C C A A A C A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C  
 C C A G G A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A  
 A G A G G G A T T C C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T  
 G G G G G G G G G C A G C A C A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C T G T  
 G C C C T G G T T C T T G C T G T C C T T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G  
 G C T T G T G G G G C C T C A G G A C G C T A C C C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A  
 C A G T G A C A T A C T C T G C C T G C C T G G G G A C A T C G T G C C T G C T C C G G G C C C C G T G C T G G C G C C  
 T A C G C A C C T G C A G A C A G A G C T G G T G C T G A G G T G C C A G A A G G A G A C C G A C T G T G A C C T C T G  
 T C T G C G T G T G G C T G T C C A C T T G G C C G T G C A T G G G C A C T G G G A A G A G C C T G A A G A T G A G G A  
 A A A G T T T G G A G G A G C A G C T G A C T C A G G G G T G G A G G A G C C T A G G A A T G C C T C T C T C C A G G C  
 C C A A G T C G T G C T C T C C T T C C A G G C C T A C C C T A C T G C C C G C T G C G T C C T G C T G G A G G T G C A  
 A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G G T A T A T G A C T G C T T  
 C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A  
 G G A A C T C A A C C A C A C A C A G C A G C T G C C T G C C C T G C C C T G G C T C A A C G T G T C A G C A G A T G G  
 T G A C A A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G T A  
 C T G G A A T C A G G T C C A G G G C C C C C A A A A C C C C G G T G G C A C A A A A A C C T G A C T G G A C C G C A  
 G A T C A T T A C C T T G A A C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A G G T G T G G C C T C T  
 G G A A C C T G A C T C C G T T A G G A C G A A C A T C T G C C C C T T C A G G G A G G A C C C C G C G C A C A C C A  
 G A A C C T C T G G C A A G C C G C C C G A C T G C G A C T G C A C C C T G C A G A G C T G G C T G C T G G A C G C  
 A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T G T G C T G G C G G G C T C C G G G T G G G G A C C C C T G  
 C C A G C C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G T C A C T G T G G A C A A G G T T C T C G A G T T  
 C C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G A A C A G C T C G G A G A A G C T G C A  
 G C T G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A A G A C G A T G T G C T A C T G T T  
 G G A G A C A C G A G G C C C C C A G G A C A A C A G A T C C C C T C T G T G C C T T G G A A C C C A G T G G C T G T A C  
 T T C A C T A C C C A G C A A A G C C T C C A C G A G G G C A G C T C G C C T T G G A G A G T A C T T A C T A C A A G A  
 C C T G C A G T C A G G C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G  
 C C C C A T G G A C A A A T A C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T  
 T G C C G C T G C G C T T T C C C T C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G  
 G C T C T T G A A A C A G G A C G T C C G C T C G G G G C G G C C G C C A G G G C C G C G C G G C T C T G C T C C T  
 C T A C T C A G C C G A T G A C T C G G G T T T C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G  
 C C A G C T G C C G C T G C G C T G G C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G  
 G C C C G T G G C T T G G T T T C A C G C G C A G C G G C G C C A G A C C C T G C A G G A G G G C G G C G T G G T G G T  
 C T T G C T C T T C T C T C C C G G T G C G G T G G C G C T G T G C A G C G A G T G G C T A C A G G A T G G G G T G T C  
 C G G G C C C G G G G C G C A C G G C C C G C A C G A C G C C T T C C G C G C C T C G C T C A G C T G C G T G C T G C C  
 C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G G G C C T G C T T C G A C A G G C T G C T  
 C C A C C C G G A C G C C G T A C C C G C C C T T T T C C G C A C C G T G C C C G T C T T C A C A C T G C C C T C C C A  
 A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C G T T C C G G G C G G C T C C A  
 A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C C A T C C  
 C C C G G G G A C T C C C G C G C C G G A C G C G G G T G G G A C C A G G G G C G G G A C C T G G G G C G G G G G A  
 C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T T C T A A A A A A A

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## FIGURE 364

MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPGLSCRLWDSIILCLPGDIVPAPGPV  
 LAPTHLQTELVLRQCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS  
 LQAQVVLSTFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR  
 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT  
 GPQIIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL  
 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE  
 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYL  
 LQDLQSGQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKG  
 WLRLKQDVRSGAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS  
 AQGPVAVFHAQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC  
 VLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSR  
 RLQERAEQVSRAALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 453-475

**N-glycosylation sites:**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241,  
 248-251, 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site:**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 552-555

**N-myristoylation sites:**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521,  
 612-617, 692-697, 696-701, 700-705

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## FIGURE 365

AATAGAAGTCCTCAGGACGGAGCAGAGGTGGCCGGCGGGCCCGGCTGACTGCGCCTCTGC  
 TTTCTTTCCATAACCTTTTCTTTCGGACTCGAATCACGGCTGCTGCGAAGGGTCTAGTTC  
 CGGACACTAGGGTGCCCGAACGCGCTGATGCCCCGAGTGCTCGCAGGGCTTCCCGCTAAC  
 CATGCTGCCGCCGCCGCGGGCCGAGCTGCCTTGCGCTGCCTGTGCTCCTGCTACTGCT  
 GGTGGTGCTGACGCCGCCCCCGACCGGCGCAAGGCCATCCCCAGGCCCAGATTACCTGCG  
 GCGCGGCTGGATGCGGCTGCTAGCGGAGGGCGAGGGCTGCGCTCCCTGCCGGCCAGAAGA  
 GTGCGCCGCGCCGCGGGGCTGCCTGCGGGCAGGGTGCGCGACGCGTGCGGCTGCTGCTG  
 GGAATGCGCCAACCTCGAGGGCCAGCTCTGCGACCTGGACCCCAGTGCTCACTTCTACGG  
 GCACTGCGGCGAGCAGCTTGAGTGCCGGCTGGACACAGGCGGCGACCTGAGCCGCGGAGA  
 GGTGCCGGAACCTCTGTGTGCCTGTCTGTCGTCGAGAGTCCGCTCTGCGGGTCCGACGGTCA  
 CACCTACTCCCAGATCTGCCGCTGCAGGAGGCGGCCCGCGCTCGGCCCCGATGCCAACCT  
 CACTGTGGCACACCCGGGGCCCTGCGAATCGGGGCCCCAGATCGTGTCACATCCATATGA  
 CACTTGGAATGTGACAGGGCAGGATGTGATCTTTGGCTGTGAAGTGTTCCTACCCCAT  
 GGCTCCCATCGAGTGAGGAAGGATGGCTTGACATCCAGCTGCCAGGGGATGACCCCCA  
 CATCTCTGTGCAGTTTAGGGGTGGACCCCAGAGGTTTGAGGTGACTGGCTGGCTGCAGAT  
 CCAGGCTGTGCGTCCAGTGATGAGGGCACTTACCGCTGCCTTGCCCGCAATGCCCTGGG  
 TCAAGTGAGGCCCCCTGCTAGCTTGACAGTGCTCACACCTGACCAGCTGAACTCTACAGG  
 CATCCCCAGCTGCGATCACTAAACCTGGTTCCCTGAGGAGGAGGCTGAGAGTGAAGAGAA  
 TGACGATTACTACTAGGTCCAGAGCTCTGGCCCATGGGGGTGGGTGAGCGGCTATAGTGT  
 TCATCCCTGCTCTTGAAAAGACCTGGAAAGGGGAGCAGGGTCCCTTCATCGACTGCTTTC  
 ATGCTGTGCTAGGGATGATCATGGGAGGCCTATTTGACTCCAAGGTAGCAGTGTGGTAG  
 GATAGAGACAAAAGCTGGAGGAGGGTAGGGAGAGAAGCTGAGACCAGGACCGGTGGGGTA  
 CAAAGGGGCCCCATGCAGGAGATGCCCTGGCCAGTAGGACCTCCAACAGGTTGTTTCCCAG  
 GCTGGGGTGGGGGCCTGAGCAGACACAGAGGTGCAGGCACCAGGATTCTCCACTTCTTCC  
 AGCCCTGCTGGGCCACAGTTCTAACTGCCCTTCTCCAGGCCCTGGTTCTTGCTATTTTC  
 CTGGTCCCCAACGTTTATCTAGCTTGTGTTGCCCTTTCCCCAACTCATCTTCCAGAACTT  
 TTCCCTCTCTCCTAAGCCCCAGTTGCACCTACTAACTGCAGTCCCTTTTGCTGTCTGCCG  
 TCTTTTGTACAAGAGAGAGAACAGCGGAGCATGACTTAGTTTCAGTGCAGAGAGATTT





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## FIGURE 367

AGACGCTACAGG**ATG**GAGCGGGGCGCAGGAGCCAAGCTGCTGCCGCTGCTGCTGCTTCTG  
 CGGGCGACTGGTTTTACATGTGCACAGACAGATGGCCGGAACGGCTACACGGCGGTCATC  
 GAAGTGACCAGCGGGGGTCCCTGGGGCGACTGGGCCTGGCCTGAGATGTGTCCCGATGGA  
 TTCTTCGCCAGCGGGTTCTCGCTCAAGGTGGAGCCTCCCCAAGGCATTCTTGCGGACGAC  
 ACTGCACTGAATGGGATCAGGCTGCACTGCGCGCGCGGGAACGTCCTAGGCAATACGCAC  
 GTGGTAGAGTCCCAGTCTGGAAGCTGGGGCGAATGGAGTGAGCCGCTGTGGTGTCGCGGC  
 GCGCCTACCTAGTGGCTTTCTCGCTTCGCGTGGAGGCACCCACGACCCTCGGTGACAAC  
 ACAGCAGCGAACAACGTGCGCTTCCGCTGTTTACAGACGGCGAGGAACTGCAGGGGCCTGGG  
 CTGAGCTGGGGAGACTTTGGAGACTGGAGTGACCATTGCCCCAAGGGCGCGTGCGGCCTG  
 CAGACCAAGATCCAGGGACCTAGAGGCCTCGGCGATGACACTGCGCTGAACGACGCGCGC  
 TTATTCTGCTGCCGCAGT**TGA**ACGGCGCCGCCGCCGCCGCTCTCTCCCGGGCCAGGAGGC  
 TAGTCCCACCTCTTGCTATTAAAGCTTCTCTGAGTTG

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## FIGURE 368

MERGAGAKLLPLLLLLRATGFTCAQTDGRNGYTAVIEVTSGGPWGDWAWPEMCPDGFFAS  
GFSLKVEPPQGIPGDDTALNGIRLHCARGNVLGNTHVVESQSGSWGGEWSEPLWCRGGAYL  
VAFSLRVEAPTTLGDNTAANNVRFRCSDGEELQGPGLSWGDFGDWSDHCPKGACGLQTKI  
QGPRGLGDDTALNDARLFCCRS

### Important features of the protein:

#### Signal peptide:

1-24

#### Transmembrane domain:

None

#### N-myristoylation site:

41-47

89-95

156-162

#### Growth factor and cytokines receptors family signature 2:

103-110

# FIGURE 369

GCCAACACTGGCCAAACCTCGGAGACCGTCCTGCGCTCTCTGGAGACGCGCTGTCCGCGC  
CCAGGGTGGTGCCATGTGGGGCGCTCGCCGCTCGTCCGTCTCCTCATCCTGGAACGCCGC  
TTCGCTCCTGCAGCTGCTGCTGGCTGCGCTGCTGGCGGCGGGGGCGAGGGCCAGCGGCGA  
GTACTGCCACGGCTGGCTGGACGCGCAGGGCGTCTGGCGCATCGGCTTCCAGTGTCCCGA  
GCGCTTCGACGGCGGCGACGCCACCATCTGCTGCGGCAGCTGCGCGTTGCGCTACTGCTG  
CTCCAGCGCCGAGGCGCGCCTGGACCAGGGCGGCTGCGACAATGACCGCCAGCAGGGCGC  
TGGCGAGCCTGGCCGGGCGGACAAAGACGGCCCCGACGGCTCGGCAGTGCCCATCTACGT  
GCCGTTCCCTCATTGTTGGCTCCGTGTTTGTGCGCCTTTATCATCTTGGGGTCCCTGGTGGC  
AGCCTGTTGCTGCAGATGTCTCCGGCCTAAGCAGGATCCCCAGCAGAGCCGAGCCCCAGG  
GGGTAACCGCTTGATGGAGACCATCCCCATGATCCCCAGTGCCAGCACCTCCCGGGGGTC  
GTCCTCACGCCAGTCCAGCACAGCTGCCAGTTCCAGCTCCAGCGCCAACTCAGGGGGCCCG  
GGCGCCCCCAACAAGGTCACAGACCAACTGTTGCTTGCCGGAAGGGACCATGAACAACGT  
GTATGTCAACATGCCCCACGAATTTCTCTGTGCTGAACTGTCAGCAGGCCACCCAGATTGT  
GCCACATCAAGGGCAGTATCTGCATCCCCCATACTGTTGGGTACACGGTGCAGCACGACTC  
TGTGCCCATGACAGCTGTGCCACCTTTCATGGACGGCCTGCAGCCTGGCTACAGGCAGAT  
TCAGTCCCCCTTCCCTCACACCAACAGTGAACAGAAGATGTACCCAGCGGTGACTGTATA  
ACCGAGAGTCACTGGTGGGTTCCTTTACTGAAGGGAGACGAAGGCAGGGGTGGATTTTCG  
AGGTGGAAGT

## FIGURE 370

MWGARRSSVSSSWNAASLLQLLLAALLAAGARASGEYCHGWLDAQGVWRIGFQCPERFDG  
 GDATEICCGSCALRYCCSSAEARLDQGGCDNDRQQGAGEPGRADKDGPDGSAVPIYVPFLI  
 VGSVFVAFIILGSLVAACCCRCLRPKQDPQQSRAPGGNRLMETIPMIPSASTSRGSSSRQ  
 SSTAASSSSSANS GARAPPTRSQTNCCLPEGTMMNNVYVNMPTNFSVLNCQQATQIVPHQG  
 QYLHPPYVG YTVQHDSVPMTAVPPFMDGLQPGYRQIQSPFPHTNSEQKMPAVTV

### Important features of the protein:

#### Signal peptide:

1-33

#### Transmembrane domain:

54-78

#### N-glycosylation site:

223-226

#### cAMP- and cGMP-dependent protein kinase phosphorylation site:

5-8

#### N-myristoylation site:

3-8, 30-35, 60-65, 86-91, 132-137, 211-216, 268-273

#### Prokaryotic membrane lipoprotein lipid attachment site:

128-138

386/392

## FIGURE 371

CACCAGACAGCACTCCAGCACTCTGTTTGGGGGGCATTTCGAAACAGCAAAATCACTCATA  
AAAGGCCAAAAAATTGCAAAAAAATAGTAATAACCAGCATGGCACTAAATAGACCATGA  
AAAGACATGTGTGTGCAGTATGAAAATTGAGACAGGAAGGCAGAGTGTCTAGCTTGTTCCTA  
CCTCAGCTGGGAATGTGCATCAGGCAACTCAAGTTTTTCACCACGGCATGTGTCTGTGAA  
TGTCCGCAAAACATTCTCTCTCCCCAGCCTTCATGTGTAACTTGGGGATGATGTGGACC  
TGGGCACTGTGGATGCTCCCTTCACTCTGCAATTCAGCCTGGCAGCTCTGCCAGCTAAG  
CCTGAGAACATTTCTCTGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCA  
GGAAAGGAAACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAA  
CATGATAAATTGTACAACCAATAGTTCTACAAGTGAAAAATCGTGCTTCGTGCTCTTTTTTC  
CTTCCAAGAATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGAT  
GGTGTAATTAATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCA  
CCTAAGATTTTCCGTGTGAAACCAGTTTTTGGGCATCAAACGAATGATTCAAATTGAATGG  
ATAAAGCCTGAGTTGGCGCCTGTTTCATCTGATTTAAAATACACACTTCGATTCAAGGACA  
GTCAACAGTACCAGCTGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAAACCA  
ACGTACAACCTCACGGGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCG  
GTCAAGGAGTCAAAGTTCTGGAGTGACTGGAGCCAAGAAAAAATGGGAATGACTGAGGAA  
GAAGCTCCATGTGGCCTGGAAGTGTGGAGAGTCTGAAACCAGCTGAGGCGGATGGAAGA  
AGGCCAGTGCGGTGTTATGGAAGAAGGCAAGAGGAGCCCCAGTCTTAGAGAAAAACACTT  
GGCTACAACATATGGTACTATCCAGAAAGCAACACTAACCTCACAGAAACAATGAACACT  
ACTAACCAGCAGCTTGAAGTGCATCTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCT  
TATAATTTCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCCAGCTATTCAAGAAAAA  
TCATTTTCACTGCATTGAGGTCATGCAGGCCCTGCGTTGCTGAGGACCAGCTAGTGGTGAAG  
TGGCAAAGCTCTGCTCTAGACGTGAACACTTGGATGATTGAATGGTTTCCGGATGTGGAC  
TCAGAGCCCAACACCCTTTCTGGAATCTGTGTCTCAGGCCACGAAGTGGACGATCCAG  
CAAGATAAATTAAACCTTTCTGGTGCTATAACATCTCTGTGTATCCAATGTTGCATGAC  
AAAGTTGGCGAGCCATATTCCATCCAGGCTTATGCCAAAGAAGGCGTTCCATCAGAAGGT  
CCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAAGAGATT  
CCCAAGAGTGAGAGAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGT  
GGAAAAGGATTCTGTAAGCACGCCCATAGCGAAGTGGAACAAAAACCCCAAGCCCCAGATA  
GATGCTATGGATAGACCTGTTGTAGGCATGGCTCCCCCATCTCATTTGTGACTTGCAACCT  
GGCATGAATCACTTAGCTTCTTTAAATCTCTCTGAAAATGGGGCCAAGAGCACCCACCTT  
TTGGGGTTTTTGGGGGTTAAATGAGAGTGAAGTGACAGTACCTGAGAGGAGAGTCTGAGG  
AAATGGAAGGAGTTGTTATAATTTGTCTGTTAGGCCCTGAATTGACCTCCCGGGAGCT  
CCCCGACCATCATTCCCAGGAATGGCGTGCCTGGCTTAAAGAGTGAGGAGGAACAGACCC  
TGTCACCATGACTTCTACTGCCCTGCCAAATCATGCTTTTGTTTTTTCAGTCCACCTTAT  
CTCCTGACATCTTAAATACTGGGCAAGGCTTGGATTCTTGCTTAGGCTAAATAATTTTTTT  
CTTATGGTAAATAACACGTAAATAATTTTTTCCAGTTTAAACATTTGAAAGTGTAATTTT  
AGTGGCATTAGAAGCATTACAAATATTGTGCAACCATCACCCTATTTCAGAACTCTTC  
TATTTCTGCCCAAATAGAAGCCCTATACCCATTATTAGTCACTCCCCATTCTCTCTCCTC  
CCACAGCCCCCTGGCAACTACCAAACCTGCTTTGTGTCTCTATGGATTGCCTATTTTGGATA  
TTTCATATACATAGAATCATAAANTAAAAA

## FIGURE 372

MCIRQLKFFTTACVCECPQNILSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENI  
SCVYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRASCSFFLPRI  
TIPDNYTIEVEAENGDGVKSHMTYWRLENIAKTEPPKIFRVKPVLGKRMIEWIKPE  
LAPVSSDLKYTLRFRTVNSTSWMEVNFANKNRKDKNQTYNLTGLQPFTEYVIALRCAVKES  
KFWSDWSQEKMGMTREEEAPCGLELWRLKPAEADGRRPVRLWKKARGAPVLEKTLGYNI  
WYYPESNTNLTETMNTTNQQLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQC  
IEVMQACVAEDQLVVKWQSSALDVNTWMIWFDPDSEPTTSLWESVSQATNWTIQQDKL  
KPFWCYNISVYPMLHDKVGEPYSIQAYAKEGVPSEGPETKVENIGVKTVTITWKEIPKSE  
RKGIIICNYTIFYQAEGGKGFCKHAHSEVEKNPKPQIDAMDRPVVGMAPP SHCDLQPGMNH  
LASLNLSENGAKSTHLLGFWGLNESEVTVPERRVLRKWKELL

### Important features of the protein:

#### Signal peptide:

1-46

#### Transmembrane domain:

None

#### N-glycosylation site:

59-63, 69-73, 99-103, 103-107, 125-129, 198-202, 215-219, 219-  
223, 309-313, 315-319, 412-416, 427-431, 487-491, 545-549, 563-  
567

#### N-myristoylation site:

32-38, 137-143, 483-489, 550-556, 561-567

#### Amidation site:

274-278

#### Growth factor and cytokines receptors family signature 1:

62-75

#### Fibronectin type III domain:

54-144  
154-247

# FIGURE 373

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCC  
 CTCGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTG  
 TGGACAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGC  
 CCCAGCAAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCAC  
 GCCTGGGCTCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCAC  
 CACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCC  
 ACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTG  
 CTGCTGATGTGGCTTCTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGC  
 CGTTAGGGTGTGTGCTGTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCTGTGCAGC  
 GTGTGTACCAGCCCTTCCCTACCACTGCGACGGGCACCGGGCCTGCAGCACCTACCGAA  
 CCATTTATAGGACCGCCTACCGCCGACGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACG  
 CGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCCTGGGGCCTGTGGAGCAGCAATAT  
 GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTG  
 CAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGCG  
 GCTGTCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGGGGGC  
 ACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCC  
 CCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGG  
 TGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGC  
 AGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGC  
 TCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCCTTCCCTGGAGGAGCAGCTGGGGTCCT  
 GCTCCTGCAAGAAAGACTCGTGAAGTGGCCAGCGCCCCAGGCTGGACTGAGCCCCCTCACGC  
 CGCCCTGCAGCCCCCATGCCCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGT  
 GACTGAGCGGAAGGCCAGGCAGGGCCTTCCCTCCTTTTCCCTCCTCCCCCTTCCCTCGGGAGG  
 GTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTTTGTGAATCCACCCCTGGCTAC  
 CCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGG  
 TACGAGTTCCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGG  
 GTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTGAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTC  
 GACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

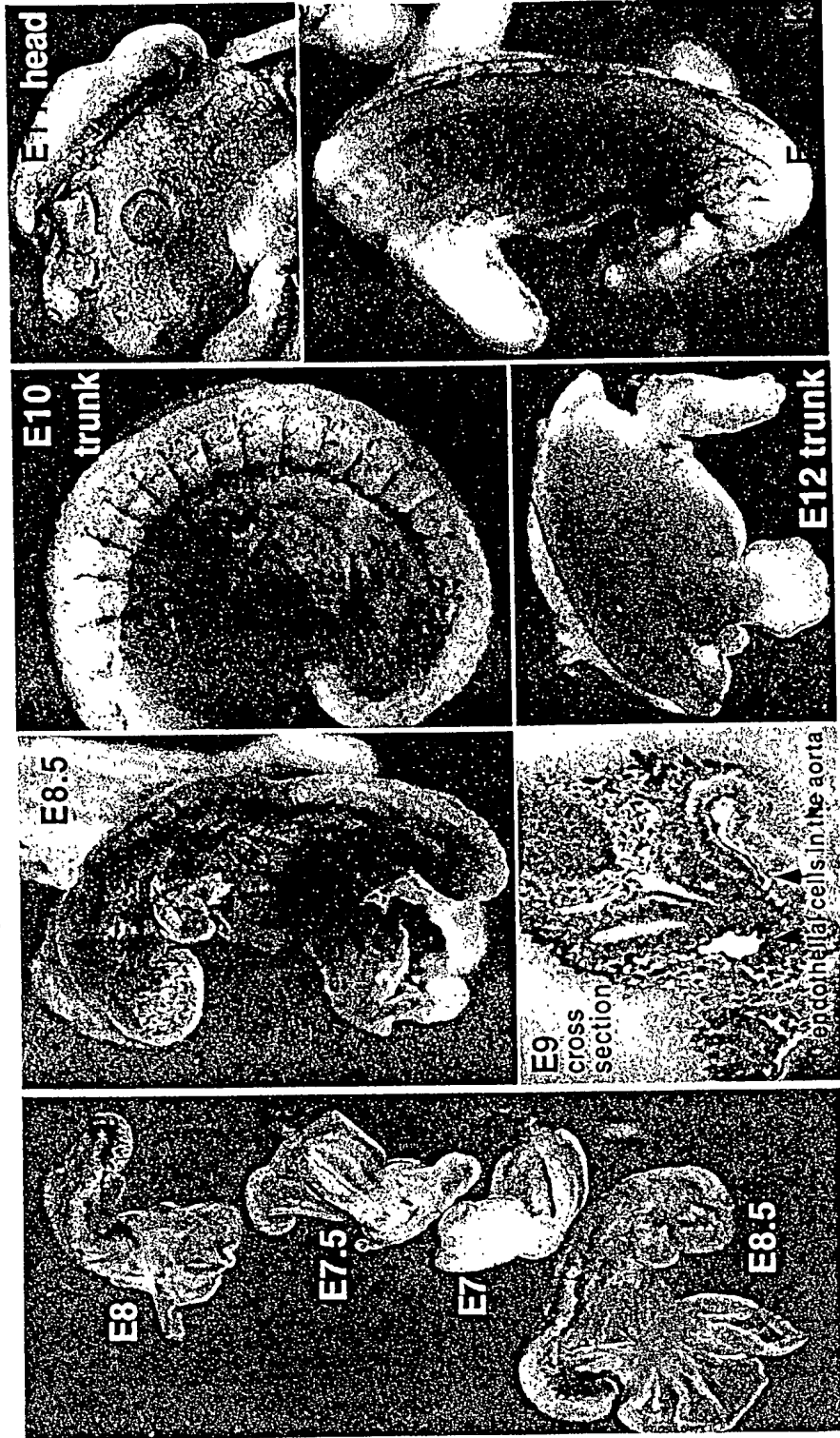
## FIGURE 374

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGD  
PVSESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGL  
PGACGAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGS  
YWCQCWEGHSLSADGTLCPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVL  
APLHSLASQALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS



FIGURE 375

Wholemound In Situ with PRO1449 Orthologue





1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809

FIGURE 377

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